GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 29, 2004, 08:37:12 ; Search time 50.5 Seconds
(without alignments)
615.450 Million cell updates/sec

Title: US-09-674-857-12
Perfect score: 583
Sequence: 1 APPVAGGPSVFLFPPKPKDT.....CKVSNKGLPSSIEKTISKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	566.5	97.2	462	2	AAW14933	Aaw14933 2A2 (Chim
2	566.5	97.2	462	2	AAW14934	Aaw14934 2A2 (Chim
3	566.5	97.2	463	2	AAW14939	Aaw14939 3F4 (Chim
4	566.5	97.2	463	2	AAW14940	Aaw14940 3F4 (Chim
5	566.5	97.2	472	5	ABP51695	Abp51695 5G1.1-TPO
6	565	96.9	110	2	AAR41717	Aar41717 Undefined
7	565	96.9	218	3	AAB07478	Aab07478 Amino aci
8	565	96.9	218	4	AAB76425	Aab76425 Human IgG
9	565	96.9	218	4	AAB67205	Aab67205 Human IgG
10	565	96.9	218	5	AAG78436	Aag78436 Native se
11	565	96.9	218	6	ABR42442	Abr42442 Human IgG
12	565	96.9	229	7	ADD32013	Add32013 Heterolog
13	565	96.9	284	6	AAE30927	Aae30927 Gly8-Glu2
14	565	96.9	327	2	AAW37346	Aaw37346 Immunoglo
15	565	96.9	327	5	AAM47859	Aam47859 Human Ig-
16	565	96.9	327	6	AAE32918	Aae32918 Human imm
17	565	96.9	327	6	AAE32630	Aae32630 Human imm
18	565	96.9	327	6	AAO30892	Aao30892 Human imm
19	565	96.9	329	2	AAW70801	Aaw70801 Amino aci
20	565	96.9	329	3	AAY92190	Aay92190 Human IgG
21	565	96.9	330	6	ABR42735	Abr42735 Anti-tiss
22	565	96.9	382	2	AAR90922	Aar90922 IL4.Y124D
23	565	96.9	382	2	AAR90921	Aar90921 IL4.Y124D
24	565	96.9	396	2	AAW10534	Aaw10534 Leptin 1-
25	565	96.9	396	2	AAW10535	Aaw10535 Leptin 1-
26	565	96.9	403	7	ADD32018	Add32018 Heterolog
27	565	96.9	432	2	AAY17903	Aay17903 Human IFN
28	565	96.9	433	2	AAW18579	Aaw18579 Interfero
29	565	96.9	443	2	AAW13564	Aaw13564 Humanised
30	565	96.9	444	2	AAY31672	Aay31672 Human IgG
31	565	96.9	444	6	ABR55342	Abr55342 Amino aci
32	565	96.9	444	7	ADC73234	Adc73234 Protein s
33	565	96.9	450	6	ABP96294	Abp96294 4A5-3.1.1
34	565	96.9	463	2	AAW14932	Aaw14932 Murine an
35	565	96.9	463	2	AAW14935	Aaw14935 2A2 Human
36	565	96.9	464	2	AAW14941	Aaw14941 3F4 Human
37	565	96.9	464	2	AAW14938	Aaw14938 Murine an
38	565	96.9	465	7	ADD93783	Add93783 Monoclona
39	565	96.9	467	2	AAR80617	Aar80617 Anti-huma
40	565	96.9	467	2	AAW14927	Aaw14927 Human gam
41	565	96.9	467	2	AAW14925	Aaw14925 Human gam
42	565	96.9	467	2	AAW14926	Aaw14926 Human gam
43	565	96.9	467	7	ADE31591	Ade31591 Gamma 4 h
44	565	96.9	467	7	ADE31593	Ade31593 Gamma 4 h
45	565	96.9	467	7	ADE31589	Ade31589 Gamma 4 h

ALIGNMENTS

RESULT 1
AAW14933
ID AAW14933 standard; protein; 462 AA.
XX
AC AAW14933;
XX
DT 17-OCT-2003 (revised)
DT 16-JUN-1997 (first entry)
XX
DE 2A2 (Chimeric) human G2/G4 chimeric antibody.
XX
KW Xenotransplantation; graft rejection; cell interaction; pig;
KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
KW chimeric antibody; diagnosis.
XX
OS Homo; sapiens.
OS Mus sp.
OS Chimeric.
XX
PN WO9711971-A1.
XX
PD 03-APR-1997.
XX
PF 27-SEP-1996; 96WO-US015575.
XX
PR 28-SEP-1995; 95US-0004489P.
PR 26-SEP-1996; 96US-00004489.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Matis LA;
XX
DR WPI; 1997-212855/19.
DR N-PSDB; AAT62931.
XX
PT Antibodies binding to porcine but not human cell interaction proteins -
PT useful to treat and assay for rejection of xenografted porcine organs,
PT tissues or cells.
XX
PS Disclosure; Page 42-44; 105pp; English.
XX
CC A chimeric antibody (AAW14933) comprises the C1 and hinge regions of
CC human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 MAb) and a
CC murine anti-porcine soluble vascular cell adhesion molecule (VCAM)
CC monoclonal antibody (MAb) 2A2 heavy chain variable region sequence (see
CC also AAW14932). The chimeric antibody is specific for porcine VCAM. It is
CC useful for diagnosing human rejection of porcine xenotransplants and for
CC improving xenotransplantation of porcine cells, tissues and organs into

```
CC   human recipients. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ   Sequence 462 AA;

  Query Match             97.2%;  Score 566.5;  DB 2;  Length 462;
  Best Local Similarity   99.1%;  Pred. No. 1.2e-48;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 305

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 355


RESULT 2
AAW14934
ID   AAW14934 standard; protein; 462 AA.
XX
AC   AAW14934;
XX
DT   17-OCT-2003  (revised)
DT   16-JUN-1997  (first entry)
XX
DE   2A2 (Chimeric) human G2/G4 chimeric antibody.
XX
KW   Xenotransplantation; graft rejection; cell interaction; pig;
KW   vascular cell adhesion molecule; VCAM; monoclonal antibody;
KW   chimeric antibody; diagnosis.
XX
OS   Homo; sapiens.
OS   Mus sp.
OS   Chimeric.
XX
PN   WO9711971-A1.
XX
PD   03-APR-1997.
XX
PF   27-SEP-1996;   96WO-US015575.
XX
PR   28-SEP-1995;   95US-0004489P.
PR   26-SEP-1996;   96US-00004489.
XX
PA   (ALEX-) ALEXION PHARM INC.
XX
PI   Mueller JP,  Evans MJ,  Mueller EE,  Rollins S,  Rother RP,  Matis LA;
XX
DR   WPI; 1997-212855/19.
DR   N-PSDB; AAT62932.
XX
PT   Antibodies binding to porcine but not human cell interaction proteins -
PT   useful to treat and assay for rejection of xenografted porcine organs,
PT   tissues or cells.
XX
PS   Disclosure; Page 44-47; 105pp; English.
XX
CC   A chimeric antibody (AAW14934) comprises the C1 and hinge regions of
CC   human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 MAb) and a
CC   murine anti-porcine soluble vascular cell adhesion molecule (VCAM)
CC   monoclonal antibody (MAb) 2A2 heavy chain variable region sequence (see
CC   also AAW14932). The chimeric antibody is specific for porcine VCAM. It is
CC   useful for diagnosing human rejection of porcine xenotransplants and for
CC   improving xenotransplantation of porcine cells, tissues and organs into
CC   human recipients. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ   Sequence 462 AA;

  Query Match             97.2%;  Score 566.5;  DB 2;  Length 462;
  Best Local Similarity   99.1%;  Pred. No. 1.2e-48;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 305

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 355


RESULT 3
AAW14939
ID   AAW14939 standard; protein; 463 AA.
XX
AC   AAW14939;
XX
DT   17-OCT-2003  (revised)
DT   16-JUN-1997  (first entry)
XX
DE   3F4 (Chimeric) human G2/G4 chimeric antibody.
XX
KW   Xenotransplantation; graft rejection; cell interaction; pig;
KW   vascular cell adhesion molecule; VCAM; monoclonal antibody;
KW   chimeric antibody; diagnosis.
XX
OS   Homo; sapiens.
OS   Mus sp.
OS   Chimeric.
XX
PN   WO9711971-A1.
XX
PD   03-APR-1997.
XX
PF   27-SEP-1996;   96WO-US015575.
XX
PR   28-SEP-1995;   95US-0004489P.
PR   26-SEP-1996;   96US-00004489.
XX
PA   (ALEX-) ALEXION PHARM INC.
XX
PI   Mueller JP,  Evans MJ,  Mueller EE,  Rollins S,  Rother RP,  Matis LA;
XX
DR   WPI; 1997-212855/19.
DR   N-PSDB; AAT62936.
XX
PT   Antibodies binding to porcine but not human cell interaction proteins -
PT   useful to treat and assay for rejection of xenografted porcine organs,
PT   tissues or cells.
XX
PS   Disclosure; Page 56-57; 105pp; English.
XX
CC   A chimeric antibody (AAW14939) comprises the C1 and hinge regions of
CC   human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 MAb) and a
CC   murine anti-porcine soluble vascular cell adhesion molecule (VCAM)
CC   monoclonal antibody (MAb) 3F4 heavy chain variable region sequence (see
CC   also AAW14938). The chimeric antibody is specific for porcine VCAM. It is
CC   useful for diagnosing human rejection of porcine xenotransplants and for
CC   improving xenotransplantation of porcine cells, tissues and organs into
CC   human recipients. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ   Sequence 463 AA;

  Query Match             97.2%;  Score 566.5;  DB 2;  Length 463;
  Best Local Similarity   99.1%;  Pred. No. 1.2e-48;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 306

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 356
```

```
RESULT 4
AAW14940
ID   AAW14940 standard; protein; 463 AA.
XX
AC   AAW14940;
XX
DT   17-OCT-2003  (revised)
DT   16-JUN-1997  (first entry)
XX
DE   3F4 (Chimeric) human G2/G4 chimeric antibody.
XX
KW   Xenotransplantation; graft rejection; cell interaction; pig;
KW   vascular cell adhesion molecule; VCAM; monoclonal antibody;
KW   chimeric antibody; diagnosis.
XX
OS   Homo; sapiens.
OS   Mus sp.
OS   Chimeric.
XX
PN   WO9711971-A1.
XX
PD   03-APR-1997.
XX
PF   27-SEP-1996;   96WO-US015575.
XX
PR   28-SEP-1995;   95US-0004489P.
PR   26-SEP-1996;   96US-00004489.
XX
PA   (ALEX-) ALEXION PHARM INC.
XX
PI   Mueller JP,  Evans MJ,  Mueller EE,  Rollins S,  Rother RP,  Matis LA;
XX
DR   WPI; 1997-212855/19.
DR   N-PSDB; AAT62937.
XX
PT   Antibodies binding to porcine but not human cell interaction proteins -
PT   useful to treat and assay for rejection of xenografted porcine organs,
PT   tissues or cells.
XX
PS   Disclosure; Page 58-61; 105pp; English.
XX
CC   A chimeric antibody (AAW14940) comprises the C1 and hinge regions of
CC   human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 MAb) and a
CC   murine anti-porcine soluble vascular cell adhesion molecule (VCAM)
CC   monoclonal antibody (MAb) 3F4 heavy chain variable region sequence (see
CC   also AAW14938). The chimeric antibody is specific for porcine VCAM. It is
CC   useful for diagnosing human rejection of porcine xenotransplants and for
CC   improving xenotransplantation of porcine cells, tissues and organs into
CC   human recipients. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ   Sequence 463 AA;

  Query Match             97.2%;  Score 566.5;  DB 2;  Length 463;
  Best Local Similarity   99.1%;  Pred. No. 1.2e-48;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 306

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 356


RESULT 5
ABP51695
ID   ABP51695 standard; protein; 472 AA.
XX
AC   ABP51695;
XX
DT   01-OCT-2002  (first entry)
XX
DE   5G1.1-TPO heavy chain amino acid sequence SEQ ID NO:67.
XX
KW   TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
KW   complementarity determining region; immunoglobin; antianaemic;
KW   haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200246238-A2.
XX
PD   13-JUN-2002.
XX
PF   05-DEC-2001; 2001WO-US047656.
XX
PR   05-DEC-2000; 2000US-0251448P.
PR   04-MAY-2001; 2001US-0288889P.
PR   29-MAY-2001; 2001US-0294068P.
XX
PA   (ALEX-) ALEXION PHARM INC.
XX
PI   Bowdish KS,  Barbas-Frederickson S,  Renshaw M;
XX
DR   WPI; 2002-566610/60.
DR   N-PSDB; ABQ73374.
XX
PT   A novel immunogen molecule comprising a region in which amino acid
PT   residues corresponding to at least a portion of the complementary
PT   determining region are replaced or fused with an erythropoietin or
PT   thrombopoetin mimetic.
XX
PS   Example 4; Fig 13A; 113pp; English.
XX
CC   The present invention describes an immunoglobin molecule or its fragment
CC   (I) comprising a region where amino acid residues corresponding to at
CC   least a portion of the complementary determining region (CDR) are
CC   replaced or fused with biologically active peptides e.g. a peptide
CC   mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
CC   that is flanked with proline at its carboxy terminus. (I) has
CC   antianaemic, haemostatic and nephrotropic activities, and can be used as
CC   a stimulator of proliferation, differentiation and maturation of
CC   haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful
CC   for stimulating proliferation, differentiation or growth of
CC   promegakaryocytes or megakaryocytes, where (I) is contacted with
CC   promegakaryocytes or megakaryocytes, which results in increased platelet
CC   production. (I) with a region where amino acid residues corresponding to
CC   a portion of CDR is replaced with an EPO mimetic, or which has one or
CC   more of its CDRs fused to an EPO mimetic, is useful for increasing the
CC   production of red blood cells, where (I) is contacted with haematopoietic
CC   stem cells or their progenitors. (I) is useful for diagnostics or
CC   therapeutics, in cell isolation strategies, and for treating patients
CC   suffering from deficiency in cell populations caused by disease,
CC   disorders or treatments related to the suppression of haematopoiesis.
CC   ABQ73288 to ABQ73377 and ABP51669 to ABP51696 represent sequences used in
CC   the exemplification of the present invention
XX
SQ   Sequence 472 AA;

  Query Match             97.2%;  Score 566.5;  DB 5;  Length 472;
  Best Local Similarity   99.1%;  Pred. No. 1.2e-48;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 315

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 365


RESULT 6
```

```
AAR41717
ID   AAR41717 standard; protein; 110 AA.
XX
AC   AAR41717;
XX
DT   25-MAR-2003  (revised)
DT   20-OCT-1993  (first entry)
XX
DE   Undefined ORF2 encoded by plasmid pAH4808.
XX
KW   Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy;
KW   light; chain; variable; constant; region; anti-human; pAH4807;
KW   transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2;
KW   endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4;
KW   diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;
KW   Parkinsons disease; Alzheimers disease; SP2/0 cell.
XX
OS   Synthetic.
XX
PN   WO9310819-A1.
XX
PD   10-JUN-1993.
XX
PF   24-NOV-1992;   92WO-US010206.
XX
PR   26-NOV-1991;   91US-00800458.
XX
PA   (ALKE-) ALKERMES INC.
XX
PI   Friden PM;
XX
DR   WPI; 1993-196742/24.
DR   N-PSDB; AAQ43848.
XX
PT   Antibody conjugates specific for transferrin receptor - used for
PT   diagnosis and treatment of cancer, AIDS and neurological disorders.
XX
PS   Disclosure; Fig 19J; 151pp; English.
XX
CC   The sequences given in AAR41715-18 are encoded by the expression vector
CC   pAH4808. This vector represents the cloning of the human gamma isotype,
CC   gamma-4, with the variable region of the murine monoclonal antibody
CC   128.1. This plasmid encodes a chimeric monoclonal antibody in which the
CC   heavy chain (VH) is derived from a murine source and the sequences
CC   encoding CH1, CH2 and CH3 are derived from a human source. This vector,
CC   in combination with the chimeric light chain vector, pAG4611 (see also
CC   AAQ43845), was transfected into SP2/0 cells and clones were isolated.
CC   128.1 is an anti-human transferrin receptor antibody which binds to the
CC   transferrin receptor on brain capillary endothelial cells. This antibody
CC   may be used in a conjugate in which it is linked to a neuropharmaceutical
CC   or diagnostic agent. The conjugate may be used to treat or prevent
CC   neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,
CC   Parkinsons and Alzheimers disease. It may also be used for diagnostic
CC   methods. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 110 AA;

  Query Match             96.9%;  Score 565;  DB 2;  Length 110;
  Best Local Similarity   97.3%;  Pred. No. 3.1e-49;
  Matches  107;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 APEPLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110


RESULT 7
AAB07478
ID   AAB07478 standard; protein; 218 AA.
XX
AC   AAB07478;
XX
DT   20-OCT-2000  (first entry)
XX
DE   Amino acid sequence of native IgG Fc region humIgG4.
XX
KW   IgG antibody; light chain; Fc region; effector function; cancer; allergy;
KW   asthma; LFA-1-mediated disorder; tumour; cancer.
XX
OS   Homo sapiens.
XX
PN   WO200042072-A2.
XX
PD   20-JUL-2000.
XX
PF   14-JAN-2000; 2000WO-US000973.
XX
PR   15-JAN-1999;   99US-0116023P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Presta LG;
XX
DR   WPI; 2000-476035/41.
XX
PT   New Fc region-containing polypeptides that have altered effector function
PT   due to one or more amino acid modifications in the Fc region, useful in
PT   the treatment of cancer and allergic conditions such as asthma.
XX
PS   Disclosure; Fig 22A; 132pp; English.
XX
CC   AAB07474-78 represent native IgG Fc regions. The proteins are used to
CC   produce Fc region-containing polypeptides that have altered effector
CC   function as a consequence of one or more amino acid modifications in the
CC   Fc region. The variant polypeptides are useful for treating cancer,
CC   allergic conditions such as asthma (with an anti-IgE antibody), and LFA-1
CC   -mediated disorders. Where the polypeptide binds the HER2 receptor, the
CC   disorder preferably is HER2-expressing cancer, e.g. a benign or malignant
CC   tumour characterized by overexpression of the HER2 receptor. Such cancers
CC   include breast cancer, squamous cell cancer, small-cell lung cancer, non-
CC   small cell lung cancer, gastrointestinal cancer, pancreatic cancer,
CC   glioblastoma, cervical cancer, ovarian cancer, bladder cancer, hepatoma,
CC   colon cancer, colorectal cancer, endometrial carcinoma, salivary gland
CC   carcinoma, kidney cancer, liver cancer, prostate cancer, vulval cancer,
CC   thyroid cancer, hepatic carcinoma and various types of head and neck
CC   cancer
XX
SQ   Sequence 218 AA;

  Query Match             96.9%;  Score 565;  DB 3;  Length 218;
  Best Local Similarity   97.3%;  Pred. No. 6.9e-49;
  Matches  107;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 61

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 111


RESULT 8
AAB76425
ID   AAB76425 standard; protein; 218 AA.
XX
AC   AAB76425;
XX
DT   10-APR-2001  (first entry)
XX
DE   Human IgG4 Fc region amino acid sequence.
XX
```

KW Human; erbB2; HER2; cancer; nervous system disease; stroke; ischaemia;
KW metabolic disorder; nutritional deficiency; Alzheimer's disease;
KW Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea;
KW Down's syndrome; nerve deafness; Meniere's disease; diabetic neuropathy.
XX
OS Homo sapiens.
XX
PN WO200101748-A2.
XX
PD 11-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-US018283.
XX
PR 02-JUL-1999; 99US-0142232P.
XX
PA (GETH) GENENTECH INC.
XX
PI Dennis MS;
XX
DR WPI; 2001-123048/13.
XX
PT Non-naturally occurring peptide ligands which compete for binding human
PT erB2 gene products, useful for treating e.g. Alzheimer's disease,
PT multiple sclerosis and diabetic neuropathy.
XX
PS Disclosure; Fig 2A; 116pp; English.
XX
CC This invention relates to non-naturally occurring peptide ligands which
CC bind to the human erbB2 gene product ErbB2 (also known as HER2). Peptides
CC represented in AAB76350 - AAB76420 and AAB76432 - AAB76509 are examples
CC of the ErbB2 binding ligands of the invention. Sequences AAB76421 -
CC AAB76431 represent antibody Fc amino acid sequences used in the isolation
CC of the peptides of the invention. The peptides compete for binding ErbB2
CC with naturally occurring ligands, and may be used to treat disorders
CC characterized by over expression of HER2/ErbB2 such as cancers, diseases
CC of the nervous system, musculature and epithelia, e.g. nervous system
CC damage resulting from trauma, surgery, strokes, ischaemia, infection,
CC metabolic disorders, nutritional deficiency or toxic agents. In
CC particular the synthetic peptide ligands may be used to treat Alzheimer's
CC disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's
CC chorea, Down's syndrome, nerve deafness, Meniere's disease and neuropathy
CC associated with diabetes
XX
SQ Sequence 218 AA;

Query Match 96.9%; Score 565; DB 4; Length 218;
Best Local Similarity 97.3%; Pred. No. 6.9e-49;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
|| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 61

Qy 61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 62 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 111

RESULT 9
AAB67205
ID AAB67205 standard; protein; 218 AA.
XX
AC AAB67205;
XX
DT 10-APR-2001 (first entry)
XX
DE Human IgG4.
XX
KW Fusion protein; immunoglobulin; multidimerization domain; ligand.
XX
OS Homo sapiens.
XX
PN WO200102440-A1.
XX
PD 11-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-US018185.
XX
PR 02-JUL-1999; 99US-0142088P.
XX
PA (GETH) GENENTECH INC.
XX
PI Dennis MS, Lazarus RA;
XX
DR WPI; 2001-123106/13.
XX
PT Novel fusion polypeptides comprising a peptide ligand domain which
PT functions to target hybrid molecule to target cell, and immunoglobulin
PT constant region multimerization domain.
XX
PS Disclosure; Fig 2; 69pp; English.
XX
CC The present invention relates to a fusion protein, comprising a peptide
CC ligand and an immunoglobulin (Ig) constant region multimerization domain
CC (Ib). The hybrid molecules comprising the peptide ligands and their
CC functional derivatives can be used in the same applications as, a peptide
CC ligand can be used. For example the peptide ligand can bind ErbB2. The
CC peptide ligand may bind to and inhibit the activity associated with a
CC particular target molecule
XX
SQ Sequence 218 AA;

Query Match 96.9%; Score 565; DB 4; Length 218;
Best Local Similarity 97.3%; Pred. No. 6.9e-49;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
|| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 61

Qy 61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 62 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 111

RESULT 10
AAG78436
ID AAG78436 standard; protein; 218 AA.
XX
AC AAG78436;
XX
DT 12-APR-2002 (first entry)
XX
DE Native sequence human IgG Fc region sequence humIgG4.
XX
KW Antibody; antigen; immunoglobin; ADCC; CDC; anti-globin response;
KW antibody dependant cell mediated cytotoxicity;
KW complement dependant cytotoxicity; epidermal growth factor receptor;
KW tumour necrosis factor; lymphocyte; tetravalent antibody; cytostatic;
KW antiinflammatory; antipsoriatic; dermatological; antiulcer;
KW antiasthmatic; antiarteriosclerotic; antirheumatic; antibacterial;
KW antiarthritic; neuroprotective; immunosuppressive; antianaemic;
KW antiallergic; antidiabetic; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO200177342-A1.
XX
PD 18-OCT-2001.
XX
PF 20-MAR-2001; 2001WO-US008928.
XX
PR 11-APR-2000; 2000US-0195819P.
XX
PA (GETH) GENENTECH INC.
XX

PI Miller KL, Presta LG;
XX
DR WPI; 2002-049149/06.
XX
PT Novel engineered antibody useful in therapeutic applications, contains a
PT dimerization domain and three or more antigen binding sites.
XX
PS Disclosure; Fig 3; 186pp; English.
XX
CC This invention relates to an isolated antibody comprising a dimerisation
CC domain and three or more antigen binding sites amino-terminal to the
CC domain. It is cytostatic, antiinflammatory, antibacterial,
CC immunosuppressive, antiallergic, an apoptosis inducer, a vaccine and used
CC in gene therapy. Along with a cytotoxic agent, is useful for treating a
CC disorder e.g. cancer in a mammal, for inducing apoptosis of a cancer
CC cell, and for killing a B cell or a cell which overexpresses or expresses
CC an ErbB receptor and for treating benign and malignant tumours,
CC inflammatory, angiogenic and immunological disorders, autoimmune
CC diseases, central nervous system inflammatory disorders. The antibody is
CC also useful for immunodiagnosis of various diseases including cancer, for
CC human therapy in redirected cytotoxicity, and also useful as fibrinolytic
CC agents or vaccine adjuvants, useful as affinity purification agent, in
CC diagnostic assays for detecting the expression of antigen of interest in
CC specific cells, tissue or serum, and useful for blocking an immune
CC response to a foreign antigen. The antigen is internalised faster than a
CC bivalent antibody by a cell expressing an antigen to which the antibodies
CC bind. The antibody comprises three or four heavy chain variable domains
CC which are able to combine with three or four light chain variable domain
CC polypeptides to form three or four antigen binding sites directed against
CC the same antigen. This sequence represents the native sequence human IgG
CC Fc region, humIgG4
XX
SQ Sequence 218 AA;

Query Match 96.9%; Score 565; DB 5; Length 218;
Best Local Similarity 97.3%; Pred. No. 6.9e-49;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
|| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 61

Qy 61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 62 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 111

RESULT 11
ABR42442
ID ABR42442 standard; protein; 218 AA.
XX
AC ABR42442;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human IgG4 Fc region.
XX
KW Human; antibody; IgG4; cytostatic; immunosuppressive; antiinflammatory;
KW antimicrobial.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 153
FT /note= "given as 'Z' in Fig 23"
XX
PN WO2003035835-A2.
XX
PD 01-MAY-2003.
XX
PF 22-OCT-2002; 2002WO-US033739.
XX
PR 25-OCT-2001; 2001US-0337642P.
XX
PR 09-JAN-2002; 2002US-0347694P.
XX
PA (GETH) GENENTECH INC.
XX
PI Presta LG;
XX
DR WPI; 2003-421421/39.
XX
PT New composition comprising a glycoprotein having a Fc region useful for
PT treating cancer, autoimmune disease, inflammatory disorder or infection
PT in a mammal.
XX
PS Disclosure; Fig 23; 139pp; English.
XX
CC The present sequence is the protein sequence of the Fc region of human
CC IgG4. A claimed composition comprises a glycoprotein having a Fc region.
CC About 80-100% of the glycoprotein comprises a mature core carbohydrate
CC structure which lacks fucose attached to the Fc region. The glycoprotein
CC preferably comprises an antibody, and the Fc region is preferably a human
CC IgG Fc region, especially a human IgG1, IgG2, IgG3 or IgG4 Fc region. The
CC glycoprotein binds FcgammaRIII with better affinity, or mediates antibody
CC -dependent cell-mediated cytotoxicity more effectively, than the
CC glycoprotein including fucose. The antibody may be chimeric, humanised or
CC human and binds a B-cell surface marker, an ErbB receptor, a tumour-
CC associated antigen or an angiogenic factor, CD20, HER2, vascular
CC endothelial growth factor, CD40 or prostate stem cell antigen. The
CC composition is useful for treating cancer, autoimmune disease, an
CC inflammatory disorder or infection in a mammal
XX
SQ Sequence 218 AA;

Query Match 96.9%; Score 565; DB 6; Length 218;
Best Local Similarity 97.3%; Pred. No. 6.9e-49;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
|| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 61

Qy 61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 62 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 111

RESULT 12
ADD32013
ID ADD32013 standard; protein; 229 AA.
XX
AC ADD32013;
XX
DT 15-JAN-2004 (first entry)
XX
DE Heterologous fusion protein related protein sequence SEQ ID NO:19.
XX
KW heterologous fusion protein;
KW hyperglycosylated granulocyte-colony stimulating factor; G-CSF;
KW human albumin; human albumin analogue; immunoglobulin; Fc;
KW immunostimulant; protein therapy; neutrophil level;
KW insufficient circulating neutrophil level;
KW chronic congenital neutropenia.
XX
OS Synthetic.
XX
PN WO2003076567-A2.
XX
PD 18-SEP-2003.
XX
PF 21-FEB-2003; 2003WO-US003120.
XX
PR 05-MAR-2002; 2002US-0361948P.
XX
PA (ELIL) LILLY & CO ELI.
XX

PI Beals JM, Kuchibhotla U;
XX
DR WPI; 2003-902770/82.
XX
PT New heterologous fusion proteins with granulocyte-colony stimulating
PT factor activity, useful for increasing neutrophil levels and treating
PT patients with low circulating neutrophils, such as after chemotherapy or
PT in neutropenia.
XX
PS Disclosure; SEQ ID NO 19; 126pp; English.
XX
CC The present invention describes a heterologous fusion protein (I)
CC comprising a hyperglycosylated granulocyte-colony stimulating factor (G-
CC CSF) analogue fused to a polypeptide having human albumin, human albumin
CC analogues, or fragments of human albumin, or the Fc portion of an
CC immunoglobulin, an analogue of the Fc portion of an immunoglobulin, or
CC fragments of the Fc portion of an immunoglobulin. Also described: (1) a
CC heterologous fusion protein, which is the product of the expression in a
CC host cell of an exogenous DNA sequence encoding (I); (2) an isolated
CC nucleic acid sequence comprising: (a) polynucleotides encoding (I); or
CC (b) a polynucleotide, which comprises any of 15 DNA sequences each
CC comprising 1044 base pairs (see ADD31996 to ADD32010), fused to the DNA
CC encoding a protein (i.e. human albumin, human albumin analogue or
CC fragments of human albumin); (3) increasing neutrophil levels in a mammal
CC comprising the administration of (I); (4) pharmaceutical formulations
CC adapted for the treatment of patients with insufficient neutrophil levels
CC comprising any of (I); (5) a vector comprising the polynucleotide of (2);
CC (6) host cells comprising the vector of (5), or expressing at least one
CC heterologous protein; and (7) producing (I). (I) has immunostimulant
CC activity, and can be used in protein therapy. (I) can be used for
CC increasing neutrophil levels in a mammal. (I) are particularly useful in
CC medicaments for the treatment of patients with insufficient circulating
CC neutrophil levels, or for the manufacture of a medicament for the
CC treatment of patients with insufficient circulating neutrophil levels.
CC The fusion protein is particularly useful for treating conditions
CC treatable by stimulation of circulating neutrophils, such as after
CC chemotherapy regimens or in chronic congenital neutropenia. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 229 AA;

Query Match 96.9%; Score 565; DB 7; Length 229;
Best Local Similarity 97.3%; Pred. No. 7.3e-49;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 APEPLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 72

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 122
```

RESULT 13
AAE30927
ID AAE30927 standard; protein; 284 AA.
XX
AC AAE30927;
XX
DT 24-FEB-2003 (first entry)
XX
DE Gly8-Glu22-GLP-1-CEx-linker-Immunoglobulin G4 (IgG4) fusion protein.
XX
KW Human; glucagon-like peptide 1; GLP-1; albumin; immunoglobulin; Ig;
KW therapy; non-insulin diabetes mellitus; obesity; antidiabetic; anorectic;
KW fusion protein.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
PN WO200246227-A2.
XX
PD 13-JUN-2002.
XX
PF 29-NOV-2001; 2001WO-US043165.
XX
PR 07-DEC-2000; 2000US-0251954P.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Glaesner W, Micanovic R, Tschang SR;
XX
DR WPI; 2003-018534/01.
XX
PT Novel heterologous fusion protein, useful for treating non-insulin
PT dependent diabetes mellitus or obesity, comprises a glucagon-like peptide
PT 1 compound fused to human albumin or to the Fc portion of an
PT immunoglobulin.
XX
PS Example 6; Page 83; 200pp; English.
XX
CC The invention relates to a heterologous fusion protein comprising a first
CC polypeptide fused to a second polypeptide, where the polypeptides has a N
CC -terminus and a C-terminus and the first polypeptide is a glucagon -like
CC peptide 1 (GLP-1) compound and the second is a human albumin or its
CC analogue or fragment, or the Fc portion of an immunoglobulin (Ig) or its
CC analogue or fragment, where the C-terminus of first polypeptide is fused
CC to the N-terminus of the second polypeptide. The invention is useful for
CC normalising blood glucose levels in mammal, for treating a patient with
CC non-insulin diabetes mellitus or obesity, or for the manufacture of
CC medicament for treating the above mentioned diseases. The present
CC sequence is GLP-1 fusion protein
XX
SQ Sequence 284 AA;

Query Match 96.9%; Score 565; DB 6; Length 284;
Best Local Similarity 97.3%; Pred. No. 9.5e-49;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 127

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 177
```

RESULT 14
AAW37346
ID AAW37346 standard; protein; 327 AA.
XX
AC AAW37346;
XX
DT 11-MAY-1998 (first entry)
XX
DE Immunoglobulin C-gamma-4 region.
XX
KW Vaccine; B-cell malignancy; lymphoma; leukaemia; tumour;
KW gene amplification; immunotherapy; therapy; immunoglobulin; C-gamma-4;
KW constant region.
XX
OS Homo sapiens.
XX
PN WO9741244-A1.
XX
PD 06-NOV-1997.
XX
PF 25-APR-1997; 97WO-US007039.
XX
PR 01-MAY-1996; 96US-00644664.
PR 06-DEC-1996; 96US-00761277.
XX
PA (GENI-) GENITOPE CORP.

XX
PI Denney DW;
XX
DR WPI; 1997-549743/50.
DR N-PSDB; AAT97189.
XX
PT Multivalent vaccine to treat B cell lymphoma or leukaemia - comprises at
PT least 2 different recombinant variable regions of immunoglobulin
PT molecules derived from B cell lymphoma cells.
XX
PS Example 10; Page 126-127; 177pp; English.
XX
CC This protein comprises an immunoglobulin (Ig) C-gamma-4 region. The
CC invention provides a method for the production of tumour- specific Ig
CC derived from a B-cell lymphoma patient. In the novel method, expression
CC plasmids containing the patient's VH region(s) joined to either a C-gamma
CC -3 (see AAT97188) or C-gamma-4 (see AAT97189) sequence and expression
CC plasmids containing the patient's VL region(s) joined to either a C-kappa
CC (see AAT97190) or C-lambda-2 (see AAT97191) sequence are cotransfected
CC along with a selectable and amplifiable marker into a cell line (e.g.
CC BW5147.G.1.4), and transfected cells are then subjected to selection and
CC amplification. The method permits the production of a multivalent vaccine
CC which reflects the degree of somatic variation found within the patient's
CC tumour. These novel multivalent vaccines provide superior vaccines for
CC the treatment of B-cell lymphoma
XX
SQ Sequence 327 AA;

Query Match 96.9%; Score 565; DB 2; Length 327;
Best Local Similarity 97.3%; Pred. No. 1.1e-48;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 170

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 220
```

RESULT 15
AAM47859
ID AAM47859 standard; protein; 327 AA.
XX
AC AAM47859;
XX
DT 22-FEB-2002 (first entry)
XX
DE Human Ig-G4 heavy chain constant region amino acid sequence.
XX
KW Human; immunoadhesin; intercellular adhesion molecule; ICAM-1;
KW human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;
KW transgenic plant.
XX
OS Homo sapiens.
XX
PN WO200183529-A2.
XX
PD 08-NOV-2001.
XX
PF 28-APR-2001; 2001WO-US013932.
XX
PR 28-APR-2000; 2000US-0200298P.
XX
PA (PLAN-) PLANET BIOTECHNOLOGY INC.
XX
PI Larrick JW, Wycoff KL;
XX
DR WPI; 2002-041481/05.
DR N-PSDB; ABA05268.
XX
PT Immunoadhesin for treating human rhinovirus infection comprises chimeric
PT intercellular adhesion molecule-1, and optionally a J chain and secretory
PT component in association.
XX
PS Disclosure; Fig 7; 138pp; English.
XX
CC The invention relates to an immunoadhesin comprising: (a) a chimeric
CC intercellular adhesion molecule (ICAM)-1 comprising a rhinovirus receptor
CC protein linked to at least a portion of an immunoglobulin heavy chain;
CC and (b) optionally a J chain and secretory component associated with the
CC chimeric ICAM-1 molecule. The immunoadhesin has plant-specific
CC glycosylation and virucide activity. The immunoadhesin is useful for
CC reducing infection by human rhinovirus (HRV) and hence the initiation or
CC spread of the common cold by HRV. The immunoadhesin binds to HRV and
CC reduces its infectivity, competing with cell surface ICAM-1 for binding
CC sites, interfering with virus entry or uncoating and directing premature
CC release of viral RNA and formation of empty capsids. Expression of the
CC immunoadhesin in plants would be tetrameric, rather than dimeric.
CC Immunoadhesin having multiple binding sites have a higher effective
CC affinity for the virus, thereby increasing the effectiveness of the
CC immunoadhesin. Association of secretory component and immunoglobulin J
CC chain increases the stability of the immunoadhesin in the mucosal
CC environment. Production is significantly less expensive in plants than in
CC animal cell culture and production in plants is safer for human use,
CC since plants are not known to harbor any animal viruses. The present
CC sequence is that of a human immunoglobulin protein sequence, useful to
CC the invention
XX
SQ Sequence 327 AA;

Query Match 96.9%; Score 565; DB 5; Length 327;
Best Local Similarity 97.3%; Pred. No. 1.1e-48;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 170

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 220
```

Search completed: April 29, 2004, 08:44:23
Job time : 52.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 29, 2004, 08:37:12 ; Search time 50.5 Seconds
(without alignments)
615.450 Million cell updates/sec

Title: US-09-674-857-3
Perfect score: 587
Sequence: 1 APPVAGGPSVFLFPPKPKDT.....CKVSNKGLPSSIEKTISKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	576	98.1	110	3	AAY54998	Aay54998 Mutated C
2	570.5	97.2	109	3	AAY54996	Aay54996 Mutated C
3	562	95.7	468	2	AAW85689	Aaw85689 D9D10 hea
4	562	95.7	488	3	AAY97175	Aay97175 Human FGF
5	562	95.7	497	3	AAY97174	Aay97174 Human FGF
6	562	95.7	525	3	AAY97173	Aay97173 Human FGF
7	562	95.7	711	2	AAW85692	Aaw85692 MoTAbII f
8	561	95.6	447	6	AAE33524	Aae33524 Human AQC
9	560	95.4	251	6	AAE35231	Aae35231 Human imm
10	558	95.1	232	5	ABB81492	Abb81492 Human mut
11	558	95.1	232	5	ABB81491	Abb81491 Human mut
12	558	95.1	250	6	AAE35220	Aae35220 Human mod
13	558	95.1	251	2	AAY05688	Aay05688 Modified
14	558	95.1	251	2	AAW97756	Aaw97756 Modified
15	558	95.1	251	3	AAB07541	Aab07541 Amino aci
16	558	95.1	251	6	AAE35218	Aae35218 Human mod
17	558	95.1	251	6	AAE35219	Aae35219 Human imm
18	558	95.1	328	5	ABB81493	Abb81493 Ztnfr12-t
19	558	95.1	332	6	AAE35228	Aae35228 Human TAC
20	558	95.1	344	6	AAE35224	Aae35224 Human TAC
21	558	95.1	348	6	AAE35225	Aae35225 Human TAC
22	558	95.1	357	6	AAE35226	Aae35226 Human TAC
23	558	95.1	392	6	AAE35223	Aae35223 Human TAC
24	558	95.1	473	5	ABB81645	Abb81645 Zcytor19
25	558	95.1	476	5	AAU76912	Aau76912 Human CRF
26	558	95.1	476	6	AAE30845	Aae30845 Human CRF
27	558	95.1	484	5	AAU76916	Aau76916 Human zcy
28	558	95.1	484	6	AAE30844	Aae30844 Human Zcy
29	558	95.1	556	5	AAE29073	Aae29073 Human IL-
30	558	95.1	559	4	AAB85286	Aab85286 IL-20RA-I
31	558	95.1	559	5	ABG67217	Abg67217 IL-20RA e
32	558	95.1	559	5	AAE23361	Aae23361 Human IL-
33	558	95.1	573	5	AAE29072	Aae29072 Human IL-
34	558	95.1	594	4	AAB85274	Aab85274 Human IL-
35	558	95.1	594	4	AAU04062	Aau04062 Human IL-
36	558	95.1	594	5	ABG67205	Abg67205 IL-20RA e
37	558	95.1	594	5	AAE23358	Aae23358 Human IL-
38	558	95.1	764	5	ABB05743	Abb05743 Human zcy
39	558	95.1	764	7	ADD68180	Add68180 Human zcy
40	557	94.9	110	2	AAR27680	Aar27680 Human imm
41	557	94.9	110	2	AAR41684	Aar41684 Undefined
42	557	94.9	116	2	AAY42621	Aay42621 Human IgG
43	557	94.9	212	2	AAR87023	Aar87023 Immunoglo
44	557	94.9	212	2	AAW02305	Aaw02305 Human IgG
45	557	94.9	212	2	AAR97264	Aar97264 Human imm

ALIGNMENTS

RESULT 1
AAY54998
ID AAY54998 standard; protein; 110 AA.
XX
AC AAY54998;
XX
DT 17-FEB-2000 (first entry)
XX
DE Mutated CH2 sequence G1deltaac.
XX
KW Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;
KW cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;
KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;
KW Crohn's disease; graft-vs-host disease; organ transplant rejection;
KW bone-marrow transplant rejection; autoimmune disease; asthma; allergy;
KW alloimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;
KW autoimmune thrombocytopaenia; arthritis; erythroblastosis foetalis;
KW neonatal alloimmune thrombocytopaenia; Goodpastures disease; therapy;
KW sickle cell anaemia; coronary artery occlusion.
XX
OS Synthetic.
XX
PN WO9958572-A1.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99WO-GB001441.
XX
PR 08-MAY-1998; 98GB-00009951.
XX
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
PI Armour KL, Clark MR, Williamson LM;
XX
DR WPI; 2000-039075/03.
XX
PT Immunoglobulic-derived binding molecules that do not activate complement
PT or trigger cytotoxic activities and maintaining desirable immunoglobulin
PT properties.
XX
PS Claim 12; Fig 17; 81pp; English.
XX
CC This sequence represents the mutated CH2 molecule G1deltaac, and is a
CC binding molecule of the invention. The recombinant binding molecule is
CC capable of binding a target molecule without triggering complement
CC dependent lysis, or the cell-mediated destruction of the target
CC comprises: (a) a binding domain capable of binding a target molecule; and
CC (b) an effector domain that is homologous to all or part of a constant

CC domain of a human immunoglobulin G (IgG) heavy chain. The binding
CC molecule is used to bind a target molecule (especially FcgammaRIIb
CC causing inhibition of B cell activation, mast cell degranulation or
CC phagocytosis). The binding molecule can be used to prevent or inhibit the
CC binding of a seccnd binding molecule, e.g. an antibody, to the target
CC molecule. The binding molecule is useful for the treatment of graft-vs-
CC host disease, organ transplant rejection, bone-marrow transplant
CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,
CC autoimmune thrombocytopaenia and arthritis), alloimmunity (e.g.
CC foetal/neonatal alloimmune thrombocytopaenia, asthma and allergy),
CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN
CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and
CC coronary artery occlusion). The binding molecules do not activate
CC complement or trigger cytotoxic activities through FcgammaR and desirable
CC IgG properties have been retained. The polypeptides do not contain non-
CC human amino acids, and are therefore likely to have reduced
CC immunogenicity. Further, they still bind Protein A, which is consistent
CC with being able to cross the human placenta through interaction with FcRn
CC (neonatal Fc receptor)
XX
SQ Sequence 110 AA;

Query Match 98.1%; Score 576; DB 3; Length 110;
Best Local Similarity 99.1%; Pred. No. 9.3e-52;
Matches 109; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 APPVAGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
```

RESULT 2
AAY54996
ID AAY54996 standard; protein; 109 AA.
XX
AC AAY54996;
XX
DT 17-FEB-2000 (first entry)
XX
DE Mutated CH2 sequence G1deltaab.
XX
KW Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;
KW cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;
KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;
KW Crohn's disease; graft-vs-host disease; organ transplant rejection;
KW bone-marrow transplant rejection; autoimmune disease; asthma; allergy;
KW alloimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;
KW autoimmune thrombocytopaenia; arthritis; erythroblastosis foetalis;
KW neonatal alloimmune thrombocytopaenia; Goodpastures disease; therapy;
KW sickle cell anaemia; coronary artery occlusion.
XX
OS Synthetic.
XX
PN WO9958572-A1.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99WO-GB001441.
XX
PR 08-MAY-1998; 98GB-00009951.
XX
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
PI Armour KL, Clark MR, Williamson LM;
XX
DR WPI; 2000-039075/03.
XX
PT Immunoglobulic-derived binding molecules that do not activate complement
PT or trigger cytotoxic activities and maintaining desirable immunoglobulin
PT properties.
XX
PS Claim 12; Fig 17; 81pp; English.
XX
CC This sequence represents the mutated CH2 molecule G1deltaab, and is a
CC binding molecule of the invention. The recombinant binding molecule is
CC capable of binding a target molecule without triggering complement
CC dependent lysis, or the cell-mediated destruction of the target
CC comprises: (a) a binding domain capable of binding a target molecule; and
CC (b) an effector domain that is homologous to all or part of a constant
CC domain of a human immunoglobulin G (IgG) heavy chain. The binding
CC molecule is used to bind a target molecule (especially FcgammaRIIb
CC causing inhibition of B cell activation, mast cell degranulation or
CC phagocytosis). The binding molecule can be used to prevent or inhibit the
CC binding of a second binding molecule, e.g. an antibody, to the target
CC molecule. The binding molecule is useful for the treatment of graft-vs-
CC host disease, organ transplant rejection, bone-marrow transplant
CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,
CC autoimmune thrombocytopaenia and arthritis), alloimmunity (e.g.
CC foetal/neonatal alloimmune thrombocytopaenia, asthma and allergy),
CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN
CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and
CC coronary artery occlusion). The binding molecules do not activate
CC complement or trigger cytotoxic activities through FcgammaR and desirable
CC IgG properties have been retained. The polypeptides do not contain non-
CC human amino acids, and are therefore likely to have reduced
CC immunogenicity. Further, they still bind Protein A, which is consistent
CC with being able to cross the human placenta through interaction with FcRn
CC (neonatal Fc receptor)
XX
SQ Sequence 109 AA;

Query Match 97.2%; Score 570.5; DB 3; Length 109;
Best Local Similarity 99.1%; Pred. No. 3.4e-51;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
```

RESULT 3
AAW85689
ID AAW85689 standard; protein; 468 AA.
XX
AC AAW85689;
XX
DT 12-AUG-1999 (first entry)
XX
DE D9D10 heavy chain fusion protein.
XX
KW Antibody; humanised; variable region; heavy chain; light chain;
KW interferon gamma; IFN; treatment; prevention; septic shock; cachexia;
KW immune disease; multiple sclerosis; Crohn's disease; skin disorders;
KW inflammation; neoplasia; dermatitis; monoclonal antibody; diabody; scFv;
KW multivalent; ruminant.
XX
OS Synthetic.
OS Mus musculus.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1. .20
FT		/note= "D9D10 light chain signal peptide"
FT	Domain	21. .137
FT		/note= "Humanised heavy chain variable domain of D9D10"
FT	Domain	138. .467
FT		/note= "Human IgG1 heavy chain constant domain"
FT	Misc-difference	468
FT		/note= "Leu added by cloning strategy"

XX
PN WO9909055-A2.
XX
PD 25-FEB-1999.
XX
PF 14-AUG-1998; 98WO-EP005165.
XX
PR 18-AUG-1997; 97EP-00870122.
PR 18-JUN-1998; 98EP-00870139.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Buyse M, Sablon E;
XX
DR WPI; 1999-180969/15.
DR N-PSDB; AAX08631.
XX
PT New engineered antibodies which bind and neutralise interferon-gamma -
PT useful for prevention and treatment of septic shock, cachexia, immune
PT diseases and skin disorders.
XX
PS Disclosure; Fig 9; 134pp; English.
XX
CC New antibodies which bind and neutralise interferon-gamma (IFN gamma) can
CC be used as a medicant, for preventing or treating septic shock, cachexia,
CC immune diseases including multiple sclerosis and Crohn's disease and skin
CC disorders including bullous, inflammatory and neoplastic dermatoses. The
CC antibody is selected from a single chain antibody (scFv), a chimeric
CC antibody or diabody comprising the humanised variable domain of the
CC monoclonal mouse anti-IFN gamma antibody D9D10; a multivalent antibody;
CC or a ruminant antibody. The antibodies are also useful for determining
CC IFN gamma levels in a sample. Two fusion cDNA genes encoding heavy and
CC light chain fusion proteins of the humanised D9D10 antibody were
CC constructed. The light chain comprised cDNA encoding the mouse D9D10
CC leader sequence, the humanised D9D10 light chain and a human
CC immunoglobulin kappa light chain constant region. The heavy chain
CC comprised cDNA encoding the mouse D9D10 light chain leader sequence
CC followed by the humanised D9D10 heavy chain variable domain and a human
CC IgG1 heavy chain constant domain in which the C1q-complement binding site
CC had been mutated. Four overlapping synthetic oligonucleotides (AAX08585-
CC 88) were used to construct the D9D10 light chain leader sequence. This
CC was then subsequently amplified using two primers (AAX08589, AAX08590) to
CC generate PCR-V fragment. The humanised heavy chain variable domain was
CC amplified from pGEM-T-VhH using two primers (AAX08591, AAX08592) to
CC generate PCR-VI fragment. The two fragments had a base pair overlap and
CC were fused together using primers (AAX08593, AAX08594) and then cloned
CC into pGEM-T to give pGEMLdrVHh. The human heavy chain constant domain was
CC amplified with two primers (AAX08595, AAX08596) and cloned into pGEM-T to
CC give pGEM-TCh. Two separate PCR amplifications were then performed using
CC pGEM-T-Ch as a template. The primers used were AAX08598, AAX08599 to
CC generate PCR-VIII fragment and AAX08597, AAX08600 to generate PCR-IX
CC fragment. These were then overlapped and fused using primers AAX08599,
CC AAX08600 and the resulting PCR-X fragment inserted into pGEMLdrVHh to
CC generate the complete heavy chain fusion DNA in a vector designated
CC pGEMhD9D10H. For a description of the construction of the light chain
CC fusion cDNA see GENESEQ records AAX08573-X08584
XX
SQ Sequence 468 AA;

Query Match 95.7%; Score 562; DB 2; Length 468;
Best Local Similarity 95.5%; Pred. No. 1.5e-49;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 310

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||| ||:|||||||||
Db        311 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK 360
```

RESULT 4

AAY97175
ID AAY97175 standard; protein; 488 AA.
XX
AC AAY97175;
XX
DT 04-DEC-2000 (first entry)
XX
DE Human FGF-RI Extracellular domain-Ig Fc fusion protein 6.
XX
KW FGF-R; fibroblast growth factor receptor; extracellular domain; IgG1;
KW immunoglobulin; G1; oligomerization domain; Fc region; fusion protein;
KW inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnerary;
KW ophthalmological; anti-proliferative.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .21
FT /label= FGF-R1_signal_peptide
FT Domain 22. .257
FT /label= FGF-R1_extracellular_domain
FT /note= "The Ig I segment and acid box are deleted"
FT Domain 59. .111
FT /label= Ig_II_segment
FT Domain 157. .222
FT /label= Ig_III_segment
FT Region 258. .488
FT /label= Human_IgG1_Fc_region
FT /note= "Contains hinge region and domains CH2 and CH3"
FT Misc-difference 276
FT /label= L276E
FT /note= "This mutation decreases the affinity of the Fc
FT portion for Fc receptors"
FT Misc-difference 376
FT /label= P376S
FT /note= "This mutation decreases the affinity of the Fc
FT portion for complement"
XX
PN WO200046380-A2.
XX
PD 10-AUG-2000.
XX
PF 07-FEB-2000; 2000WO-US003166.
XX
PR 08-FEB-1999; 99US-0119002P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Kavanaugh WM, Ballinger M;
XX
DR WPI; 2000-514961/46.
DR N-PSDB; AAA52132.
XX
PT New polypeptide comprising a fibroblast growth factor receptor
PT extracellular domain fused to a heterologous oligomerization domain for
PT treating FGF-, angiogenesis-, or FGF receptor-mediated disorders.
XX
PS Claim 14; Page 68-69; 70pp; English.
XX
CC Novel fusion protein constructs comprise a fibroblast growth factor (FGF)
CC receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin
CC (Ig) I segment fused to a heterologous oligomerization domain that
CC comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4
CC region, or light chain of an immunoglobulin molecule, or a peptide with a
CC leucine zipper motif. The Ig I segment is not necessary for binding of
CC acidic FGF and basic FGF (bFGF). The Ig I deletion further increases the
CC affinity for aFGF and heparin, protects the core of the molecule from
CC proteolysis, and abrogates the heparin requirement for aFGF binding. The
CC new fusion polypeptides are better FGF inhibitors than FGF-R monomer
CC proteins. The FGFR-Ig Fc fusion dimers are active as FGF antagonists at
CC subnanomolar concentrations and were 20-fold more potent than the FGF-R
CC monomer protein as competitors of bFGF binding to immobilized FGF-Rs. The
CC fusion constructs are useful to treat FGF-, angiogenesis-, or FGF-R-

```
CC   mediated disorders, such as tumourigenesis (e.g. bladder, breast, lung,
CC   rectal, testis and cervical tumours), neovascularization (e.g. diabetic
CC   retinopathy, neovascular glaucoma, wound healing and corneal scarring)
CC   and hyper-proliferation of vascular smooth muscle cells (e.g.
CC   postangioplasty and postatherectomy restenosis)
XX
SQ   Sequence 488 AA;

  Query Match             95.7%;  Score 562;  DB 3;  Length 488;
  Best Local Similarity   95.5%;  Pred. No. 1.6e-49;
  Matches  105;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 APELEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 331

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||| ||:||||||||||
Db        332 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK 381


RESULT 5
AAY97174
ID   AAY97174 standard; protein; 497 AA.
XX
AC   AAY97174;
XX
DT   04-DEC-2000  (first entry)
XX
DE   Human FGF-RI Extracellular domain-Ig Fc fusion protein 5.
XX
KW   FGF-R; fibroblast growth factor receptor; extracellular domain; IgG1;
KW   immunoglobulin; G1; oligomerization domain; Fc region; fusion protein;
KW   inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnerary;
KW   ophthalmological; anti-proliferative.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .21
FT                   /label= FGF-R1_signal_peptide
FT   Domain          22. .257
FT                   /label= FGF-R1_extracellular_domain
FT                   /note= "The Ig I segment and acid box are deleted"
FT   Domain          59. .111
FT                   /label= Ig_II_segment
FT   Domain          157. .222
FT                   /label= Ig_III_segment
FT   Peptide         258. .265
FT                   /label= Linker
FT   Region          266. .497
FT                   /label= Human_IgG1_Fc_region
FT                   /note= "Contains hinge region and domains CH2 and CH3"
FT   Misc-difference 285
FT                   /label= L285E
FT                   /note= "This mutation decreases the affinity of the Fc
FT                   portion for Fc receptors"
FT   Misc-difference 385
FT                   /label= P385S
FT                   /note= "This mutation decreases the affinity of the Fc
FT                   portion for complement"
XX
PN   WO200046380-A2.
XX
PD   10-AUG-2000.
XX
PF   07-FEB-2000; 2000WO-US003166.
XX
PR   08-FEB-1999;   99US-0119002P.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Kavanaugh WM,  Ballinger M;
XX
DR   WPI; 2000-514961/46.
DR   N-PSDB; AAA52131.
XX
PT   New polypeptide comprising a fibroblast growth factor receptor
PT   extracellular domain fused to a heterologous oligomerization domain for
PT   treating FGF-, angiogenesis-, or FGF receptor-mediated disorders.
XX
PS   Claim 14; Page 65-66; 70pp; English.
XX
CC   Novel fusion protein constructs comprise a fibroblast growth factor (FGF)
CC   receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin
CC   (Ig) I segment fused to a heterologous oligomerization domain that
CC   comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4
CC   region, or light chain of an immunoglobulin molecule, or a peptide with a
CC   leucine zipper motif. The Ig I segment is not necessary for binding of
CC   acidic FGF and basic FGF (bFGF). The Ig I deletion further increases the
CC   affinity for aFGF and heparin, protects the core of the molecule from
CC   proteolysis, and abrogates the heparin requirement for aFGF binding. The
CC   new fusion polypeptides are better FGF inhibitors than FGF-R monomer
CC   proteins. The FGFR-Ig Fc fusion dimers are active as FGF antagonists at
CC   subnanomolar concentrations and were 20-fold more potent than the FGF-R
CC   monomer protein as competitors of bFGF binding to immobilized FGF-Rs. The
CC   fusion constructs are useful to treat FGF-, angiogenesis-, or FGF-R-
CC   mediated disorders, such as tumourigenesis (e.g. bladder, breast, lung,
CC   rectal, testis and cervical tumours), neovascularization (e.g. diabetic
CC   retinopathy, neovascular glaucoma, wound healing and corneal scarring)
CC   and hyper-proliferation of vascular smooth muscle cells (e.g.
CC   postangioplasty and postatherectomy restenosis)
XX
SQ   Sequence 497 AA;

  Query Match             95.7%;  Score 562;  DB 3;  Length 497;
  Best Local Similarity   95.5%;  Pred. No. 1.6e-49;
  Matches  105;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 APELEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 340

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||| ||:||||||||||
Db        341 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK 390


RESULT 6
AAY97173
ID   AAY97173 standard; protein; 525 AA.
XX
AC   AAY97173;
XX
DT   04-DEC-2000  (first entry)
XX
DE   Human FGF-RI Extracellular domain-Ig Fc fusion protein 4.
XX
KW   FGF-R; fibroblast growth factor receptor; extracellular domain; IgG1;
KW   immunoglobulin; G1; oligomerization domain; Fc region; fusion protein;
KW   inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnerary;
KW   ophthalmological; anti-proliferative.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .21
FT                   /label= FGF-R1_signal_peptide
FT   Domain          22. .285
FT                   /label= FGF-R1_extracellular_domain
FT                   /note= "Ig I segment is deleted"
FT   Domain          37. .44
FT                   /label= Acid_box_segment
FT   Domain          87. .139
FT                   /label= Ig_II_segment
FT   Peptide         286. .293
```

```
FT                   /label= Linker
FT   Region          294. .525
FT                   /label= Human_IgG1_Fc_region
FT                   /note= "Contains hinge region and domains CH2 and CH3"
FT   Misc-difference 313
FT                   /label= L313E
FT                   /note= "The mutation decreases the affinity of the Fc
FT                   portion for Fc receptors"
FT   Misc-difference 409
FT                   /label= P409S
FT                   /note= "The mutation decreases the affinity of the Fc
FT                   portion for complement"
FT   Domain          445. .250
FT                   /label= Ig_III_segment
XX
PN   WO200046380-A2.
XX
PD   10-AUG-2000.
XX
PF   07-FEB-2000; 2000WO-US003166.
XX
PR   08-FEB-1999;   99US-0119002P.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Kavanaugh WM,  Ballinger M;
XX
DR   WPI; 2000-514961/46.
DR   N-PSDB; AAA52130.
XX
PT   New polypeptide comprising a fibroblast growth factor receptor
PT   extracellular domain fused to a heterologous oligomerization domain for
PT   treating FGF-, angiogenesis-, or FGF receptor-mediated disorders.
XX
PS   Claim 14; Page 61-62; 70pp; English.
XX
CC   Novel fusion protein constructs comprise a fibroblast growth factor (FGF)
CC   receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin
CC   (Ig) I segment fused to a heterologous oligomerization domain that
CC   comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4
CC   region, or light chain of an immunoglobulin molecule, or a peptide with a
CC   leucine zipper motif. The Ig I segment is not necessary for binding of
CC   acidic FGF and basic FGF (bFGF). The Ig I deletion further increases the
CC   affinity for aFGF and heparin, protects the core of the molecule from
CC   proteolysis, and abrogates the heparin requirement for aFGF binding. The
CC   new fusion polypeptides are better FGF inhibitors than FGF-R monomer
CC   proteins. The FGFR-Ig Fc fusion dimers are active as FGF antagonists at
CC   subnanomolar concentrations and were 20-fold more potent than the FGF-R
CC   monomer protein as competitors of bFGF binding to immobilized FGF-Rs. The
CC   fusion constructs are useful to treat FGF-, angiogenesis-, or FGF-R-
CC   mediated disorders, such as tumourigenesis (e.g. bladder, breast, lung,
CC   rectal, testis and cervical tumours), neovascularization (e.g. diabetic
CC   retinopathy, neovascular glaucoma, wound healing and corneal scarring)
CC   and hyper-proliferation of vascular smooth muscle cells (e.g.
CC   postangioplasty and postatherectomy restenosis)
XX
SQ   Sequence 525 AA;

  Query Match             95.7%;  Score 562;  DB 3;  Length 525;
  Best Local Similarity   95.5%;  Pred. No. 1.8e-49;
  Matches  105;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 APELEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 368

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||| ||:|||||||||||
Db        369 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK 418


RESULT 7
AAW85692
```

```
ID   AAW85692 standard; protein; 711 AA.
XX
AC   AAW85692;
XX
DT   12-AUG-1999  (first entry)
XX
DE   MoTAbII fusion protein.
XX
KW   Antibody; humanised; variable region; heavy chain; light chain;
KW   interferon gamma; IFN; treatment; prevention; septic shock; cachexia;
KW   immune disease; multiple sclerosis; Crohn's disease; skin disorders;
KW   inflammation; neoplasia; dermatitis; monoclonal antibody; diabody; scFv;
KW   multivalent; ruminant.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .20
FT                   /label= Mouse_D9D10_light_chain_signal_peptide
FT   Domain          21. .137
FT                   /note= "Humanised heavy chain variable domain of D9D10"
FT   Domain          138. .467
FT                   /note= "Human IgG1 heavy chain constant domain"
FT   Misc-difference 468
FT                   /note= "Leu added by cloning strategy"
FT   Region          469. .472
FT                   /label= Gly(3)Ser_linker
FT   Domain          473. .711
FT                   /label= Humanised)_D9D10_ScFv
XX
PN   WO9909055-A2.
XX
PD   25-FEB-1999.
XX
PF   14-AUG-1998;   98WO-EP005165.
XX
PR   18-AUG-1997;   97EP-00870122.
PR   18-JUN-1998;   98EP-00870139.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   Buyse M,  Sablon E;
XX
DR   WPI; 1999-180969/15.
DR   N-PSDB; AAW85692.
XX
PT   New engineered antibodies which bind and neutralise interferon-gamma -
PT   useful for prevention and treatment of septic shock, cachexia, immune
PT   diseases and skin disorders.
XX
PS   Disclosure; Fig 20; 134pp; English.
XX
CC   New antibodies which bind and neutralise interferon-gamma (IFN gamma) can
CC   be used as a medicant, for preventing or treating septic shock, cachexia,
CC   immune diseases including multiple sclerosis and Crohn's disease and skin
CC   disorders including bullous, inflammatory and neoplastic dermatoses. The
CC   antibody is selected from a single chain antibody (scFv), a chimeric
CC   antibody or diabody comprising the humanised variable domain of the
CC   monoclonal mouse anti-IFN gamma antibody D9D10; a multivalent antibody;
CC   or a ruminant antibody. The antibodies are also useful for determining
CC   IFN gamma levels in a sample
XX
SQ   Sequence 711 AA;

  Query Match             95.7%;  Score 562;  DB 2;  Length 711;
  Best Local Similarity   95.5%;  Pred. No. 2.5e-49;
  Matches  105;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 310

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
```

```
                     ||||||||||||||||||||||||||||||||||||||||||| ||:||||||||||
Db        311 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK 360
```

RESULT 8
AAE33524
ID AAE33524 standard; protein; 447 AA.
XX
AC AAE33524;
XX
DT 02-APR-2003 (first entry)
XX
DE Human AQC2 heavy chain mutant protein, hsAQC2.
XX
KW Human; very late activation antigen; VLA-1; beta1 containing integrin;
KW immunological disorder; inflammatory disorder; skin related condition;
KW psoriasis; eczema; burn; dermatitis; respiratory distress syndrome;
KW fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis;
KW fever; migraine headache; inflammatory bowel disease; Crohn's disease;
KW irritable bowel syndrome; colitis; colorectal cancer; vascular disease;
KW atherosclerosis; thyroiditis; aplastic anaemia; periarteritis nodosa;
KW gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease;
KW osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis;
KW systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome;
KW renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis;
KW hypersensitivity; graft rejection; transplant rejection; conjunctivitis;
KW graft versus host disease; myocardial ischaemia; mutant; mutein.
XX
OS Homo sapiens.
XX
PN WO200283854-A2.
XX
PD 24-OCT-2002.
XX
PF 12-APR-2002; 2002WO-US011521.
XX
PR 13-APR-2001; 2001US-0283794P.
PR 06-JUL-2001; 2001US-0303689P.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Lyne PD, Garber EA, Saldanha JW, Karpusas M;
XX
DR WPI; 2003-093009/08.
XX
PT New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
PT mediated immunological or inflammatory disorders, e.g. psoriasis, eczema,
PT burns, dermatitis, and abnormal proliferation of hair follicle cells or
PT fibrosis.
XX
PS Example 23; Page 92; 248pp; English.
XX
CC The present invention relates to novel antibodies that specifically bind
CC to very late activation (VLA-1; beta1 containing integrins) antigens and
CC methods of using these antibodies to treat immunological disorders. The
CC anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
CC mediated immunological or inflammatory disorders such as skin related
CC conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal
CC proliferation of hair follicle cells), fibrosis (e.g. kidney or lung
CC fibrosis), allergic rhinitis, respiratory distress syndrome, asthma,
CC bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-
CC intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease,
CC gastritis, irritable bowel syndrome, colitis and colorectal cancer),
CC vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia,
CC periarteritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,
CC autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid
CC arthritis, systemic lupus erythematosus and multiple sclerosis), renal
CC failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,
CC polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or
CC immediate hypersensitivity), graft and transplant rejections, graft
CC versus host disease, conjunctivitis, swelling occurring after injury,
CC myocardial ischaemia or endotoxin shock syndrome. The present sequence is
CC human AQC2 heavy chain mutant protein, hsAQC2
XX
SQ Sequence 447 AA;

```
  Query Match             95.6%;  Score 561;  DB 6;  Length 447;
  Best Local Similarity   95.5%;  Pred. No. 1.8e-49;
  Matches  105;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 291

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||| ||: ||||||||||
Db        292 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 341
```

RESULT 9
AAE35231
ID AAE35231 standard; protein; 251 AA.
XX
AC AAE35231;
XX
DT 28-MAY-2003 (first entry)
XX
DE Human immunoglobulin gamma1 mutant protein, A134S.
XX
KW Transmembrane activator; calcium modulator; nephrotropic; antibacterial;
KW TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
KW anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;
KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;
KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;
KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;
KW mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Binding-site 38. .41
FT /note= "FcgammaRI binding site"
FT Misc-difference 134
FT /note= "Wild-type Ala is replaced with Ser"
XX
PN WO200294852-A2.
XX
PD 28-NOV-2002.
XX
PF 20-MAY-2002; 2002WO-US015910.
XX
PR 24-MAY-2001; 2001US-0293343P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Rixon MW, Gross JA;
XX
DR WPI; 2003-148455/14.
XX
PT Transmembrane activator and calcium modulator and cyclophilin ligand-
PT interactor (TACI)-immunoglobulin fusion protein, for treating cancer or
PT diabetes, comprises a TACI receptor group and an immunoglobulin group.
XX
PS Example 1; Col; 71pp; English.
XX
CC The invention relates to fusion proteins comprising transmembrane
CC activator and calcium modulator and cyclophilin ligand-interactor (TACI)
CC receptor group that binds tumour necrosis factor-like protein (ZTNF)2 or
CC ZTNF4; and an immunoglobulin group comprising a constant region of an
CC immunoglobulin. The invention is used to manufacture a medicament for
CC inhibiting the proliferation of tumour cells in a mammalian subject. The
CC composition comprising the fusion protein may also be used in treating
CC autoimmune diseases (e.g. systemic lupus erythematosus, multiple
CC sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal

CC diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft
CC rejection, anaemia and septic shock. The fusion proteins are also used in
CC gene therapy. The present sequence is human immunoglobulin gammal mutant
CC protein. This sequence is used in the exemplification of the invention.
CC Note: This sequence is not shown in the specification, however it is
CC constructed based on human immunoglobulin gammal protein (SEQ ID NO:6)
CC sequence shown in column 92-93 (AAE35214)
XX
SQ Sequence 251 AA;

Query Match 95.4%; Score 560; DB 6; Length 251;
Best Local Similarity 95.5%; Pred. No. 1.1e-49;
Matches 105; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 35 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 94

Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
Db 95 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSPIEKTISKAK 144

RESULT 10
ABB81492
ID ABB81492 standard; protein; 232 AA.
XX
AC ABB81492;
XX
DT 02-SEP-2002 (first entry)
XX
DE Human mutated Fc protein designated Fc5 SEQ ID NO:32.
XX
KW Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
KW light chain neuropathy; hypertension; large vessel disease;
KW graft-versus host disease; graft rejection; Crohn's disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200238766-A2.
XX
PD 16-MAY-2002.
XX
PF 05-NOV-2001; 2001WO-US047018.
XX
PR 07-NOV-2000; 2000US-0246449P.
PR 20-DEC-2000; 2000US-0257131P.
PR 28-JUN-2001; 2001US-0301715P.
PR 29-AUG-2001; 2001US-0315565P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Gross JA, Xu W, Henne RM, Grant FJ;
XX
DR WPI; 2002-508212/54.
DR N-PSDB; ABN89447.
XX
PT Novel isolated human tumor necrosis factor receptor polypeptide, termed
PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage
PT renal failure or renal disease and lymphoma.
XX
PS Example 4; Page 148-149; 154pp; English.
XX
CC The present invention describes a human tumour necrosis factor receptor
CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,
CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
CC activities, and can be used in gene therapy. (I) can be used for
CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
CC (e.g. ZTNF4), for treating disorders and diseases associated with B
CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
CC inhibiting the proliferation of tumour cells. (I) is useful for treating
CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
CC leukaemia, nephritis, and pyelonephritis, and for treating renal
CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
CC amyloidosis, hypertension, large vessel diseases, graft-versus host
CC disease, graft rejection and Crohn's disease. (I) is useful for
CC modulating the immune system, for regulating B cell responses and
CC development, for modulating development of other cells, antibody
CC production and cytokine production, and for modulating T and B cell
CC communication. Human Ztnfr12 is located to chromosome 22q13.2. The
CC present sequence represents a mutated Fc protein designated Fc5, which is
CC used in an example from the present invention
XX
SQ Sequence 232 AA;

Query Match 95.1%; Score 558; DB 5; Length 232;
Best Local Similarity 95.5%; Pred. No. 1.7e-49;
Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 16 APEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 75

Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
Db 76 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAK 125

RESULT 11
ABB81491
ID ABB81491 standard; protein; 232 AA.
XX
AC ABB81491;
XX
DT 02-SEP-2002 (first entry)
XX
DE Human mutated Fc designated Fc4 protein SEQ ID NO:28.
XX
KW Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
KW light chain neuropathy; hypertension; large vessel disease;
KW graft-versus host disease; graft rejection; Crohn's disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200238766-A2.
XX
PD 16-MAY-2002.
XX
PF 05-NOV-2001; 2001WO-US047018.
XX
PR 07-NOV-2000; 2000US-0246449P.
PR 20-DEC-2000; 2000US-0257131P.
PR 28-JUN-2001; 2001US-0301715P.
PR 29-AUG-2001; 2001US-0315565P.

XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Gross JA, Xu W, Henne RM, Grant FJ;
XX
DR WPI; 2002-508212/54.
DR N-PSDB; ABN89444.
XX
PT Novel isolated human tumor necrosis factor receptor polypeptide, termed
PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage
PT renal failure or renal disease and lymphoma.
XX
PS Example 4; Page 146; 154pp; English.
XX
CC The present invention describes a human tumour necrosis factor receptor
CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,
CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
CC activities, and can be used in gene therapy. (I) can be used for
CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
CC (e.g. ZTNF4), for treating disorders and diseases associated with B
CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
CC inhibiting the proliferation of tumour cells. (I) is useful for treating
CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
CC leukaemia, nephritis, and pyelonephritis, and for treating renal
CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
CC amyloidosis, hypertension, large vessel diseases, graft-versus host
CC disease, graft rejection and Crohn's disease. (I) is useful for
CC modulating the immune system, for regulating B cell responses and
CC development, for modulating development of other cells, antibody
CC production and cytokine production, and for modulating T and B cell
CC communication. Human Ztnfr12 is located to chromosome 22q13.2. The
CC present sequence represents a mutated Fc protein designated Fc4, which is
CC used in an example from the present invention
XX
SQ Sequence 232 AA;

Query Match 95.1%; Score 558; DB 5; Length 232;
Best Local Similarity 95.5%; Pred. No. 1.7e-49;
Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              ||    | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 APEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 75

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||| ||||||||||||
Db         76 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAK 125
```

RESULT 12
AAE35220
ID AAE35220 standard; protein; 250 AA.
XX
AC AAE35220;
XX
DT 28-MAY-2003 (first entry)
XX
DE Human modified immunoglobulin moiety #3.
XX
KW Transmembrane activator; calcium modulator; nephrotropic; antibacterial;
KW TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
KW anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;
KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;
KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;
KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200294852-A2.
XX
PD 28-NOV-2002.
XX
PF 20-MAY-2002; 2002WO-US015910.
XX
PR 24-MAY-2001; 2001US-0293343P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Rixon MW, Gross JA;
XX
DR WPI; 2003-148455/14.
DR N-PSDB; AAD53758.
XX
PT Transmembrane activator and calcium modulator and cyclophilin ligand-
PT interactor (TACI)-immunoglobulin fusion protein, for treating cancer or
PT diabetes, comprises a TACI receptor group and an immunoglobulin group.
XX
PS Disclosure; Col 110-111; 71pp; English.
XX
CC The invention relates to fusion proteins comprising transmembrane
CC activator and calcium modulator and cyclophilin ligand-interactor (TACI)
CC receptor group that binds tumour necrosis factor-like protein (ZTNF)2 or
CC ZTNF4; and an immunoglobulin group comprising a constant region of an
CC immunoglobulin. The invention is used to manufacture a medicament for
CC inhibiting the proliferation of tumour cells in a mammalian subject. The
CC composition comprising the fusion protein may also be used in treating
CC autoimmune diseases (e.g. systemic lupus erythematosus, multiple
CC sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal
CC diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft
CC rejection, anaemia and septic shock. The fusion proteins are also used in
CC gene therapy. The present sequence is human modified immunoglobulin
CC moiety used in the invention
XX
SQ Sequence 250 AA;

Query Match 95.1%; Score 558; DB 6; Length 250;
Best Local Similarity 95.5%; Pred. No. 1.8e-49;
Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              ||    | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         35 APEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 94

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||| ||||||||||||
Db         95 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAK 144
```

RESULT 13
AAY05688
ID AAY05688 standard; protein; 251 AA.
XX
AC AAY05688;
XX
DT 19-JUL-1999 (first entry)
XX
DE Modified human IgG Fc sequence.
XX
KW ZTNFR-6; tumour necrosis factor receptor-6; human; IgG1; Fc region;
KW cell maturation; bone cell regulation; mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 38
FT /note= "Leu in native sequence"
FT Misc-difference 39
FT /note= "Leu in native sequence"
FT Misc-difference 41

FT /note= "Gly in native sequence"
FT Misc-difference 134
FT /note= "Ala in native sequence"
FT Misc-difference 135
FT /note= "Pro in native sequence"
XX
PN WO9911790-A1.
XX
PD 11-MAR-1999.
XX
PF 03-SEP-1998; 98WO-US018364.
XX
PR 04-SEP-1997; 97US-0057608P.
PR 04-SEP-1997; 97US-00923725.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Farrah TM, Gross JA, Matthews SM;
XX
DR WPI; 1999-205190/17.
DR N-PSDB; AAX25272.
XX
PT New secreted or membrane bound tumor necrosis factor receptor ZTNFR-6 -
PT useful for detecting a genetic abnormality in a patient.
XX
PS Example 4; Page 138-139; 145pp; English.
XX
CC The present sequence represents a modified human IgG1 Fc region in which
CC the FcgRI binding site has been mutated from Leu-Leu-Gly-Gly to Ala-Glu-
CC Glu-Ala in order to reduce FcR1 binding, and residues Ala-134 and Pro-135
CC have been altered to Ser-134 and Ser-135 to reduce complement C1q binding
CC and/or complement fixation. The mutations were introduced into the native
CC Fc DNA sequence by PCR-mediated mutagenesis (see also AAX25272). The
CC construct was utilised in the preparation of ZTNFR-6-Ig fusion vectors.
CC Soluble ZTNFR-6 (see AAY05679) was expressed in BHK 570 mammalian cells
CC and also in baculovirus-infected Spodoptera frugiperda Sf9 insect cells.
CC ZTNFR-6 is a novel human tumour necrosis factor receptor. ZTNFR-6
CC polypeptides are useful for promoting cellular maturation and bone cell
CC regulation
XX
SQ Sequence 251 AA;

Query Match 95.1%; Score 558; DB 2; Length 251;
Best Local Similarity 95.5%; Pred. No. 1.8e-49;
Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 35 APEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 94

Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
Db 95 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAK 144

RESULT 14
AAW97756
ID AAW97756 standard; protein; 251 AA.
XX
AC AAW97756;
XX
DT 21-MAY-1999 (first entry)
XX
DE Modified human IgG1 Fc region.
XX
KW ZTNFR-5; tumour necrosis factor receptor; TNFR; human; cell maturation;
KW bone cell regulation; IgG1; immunoglobulin; fusion protein; mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9904001-A1.
XX
PD 28-JAN-1999.
XX
PF 21-JUL-1998; 98WO-US015072.
XX
PR 21-JUL-1997; 97US-0053203P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Farrah TM;
XX
DR WPI; 1999-132245/11.
DR N-PSDB; AAX07232.
XX
PT Novel tumour necrosis factor receptor ZTNFR5 - useful for regulating
PT maturation of TNF-ligand bearing cells.
XX
PS Example 3; Page 90-92; 109pp; English.
XX
CC This polypeptide comprises a modified human IgG1 Fc region. IgFc cDNA was
CC amplified from a human foetal liver library by PCR (see AAX07230-31). PCR
CC was also used to introduce mutations within the Fc region to reduce FcgRI
CC binding, and to introduce A134S and P135S mutations to reduce complement
CC C1q binding and/or complement fixation (see also AAX07232). Mammalian and
CC baculovirus expression vectors for soluble mutated IgFc were prepared,
CC and used to construct ZTNFR-5-mutated IgFc fusion vectors. ZTNFR-5 (see
CC AAW97749) is a novel human tumour necrosis factor receptor ZTNFR-5. ZTNFR
CC -5 polypeptides and nucleic acids (see AAX07226) can be used to screen
CC for ligands, agonists and antagonists of ZTNFR-5. The polypeptides can be
CC used in bone cell regulation and to regulate the maturation of TNF ligand
CC -bearing cells
XX
SQ Sequence 251 AA;

Query Match 95.1%; Score 558; DB 2; Length 251;
Best Local Similarity 95.5%; Pred. No. 1.8e-49;
Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 35 APEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 94

Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
Db 95 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAK 144

RESULT 15
AAB07541
ID AAB07541 standard; protein; 251 AA.
XX
AC AAB07541;
XX
DT 20-OCT-2000 (first entry)
XX
DE Amino acid sequence of the human Fc region.
XX
KW Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
KW ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
KW renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
KW immune response; immunosuppression; graft rejection; joint pain;
KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
KW renal artery stenosis; occlusion; cholesterol; renal emboli.
XX
OS Homo sapiens.
XX
PN WO200040716-A2.
XX
PD 13-JUL-2000.

XX
PF 07-JAN-2000; 2000WO-US000396.
XX
PR 07-JAN-1999; 99US-00226533.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Gross JA, Xu W, Madden K, Yee DP;
XX
DR WPI; 2000-452538/39.
DR N-PSDB; AAA58591.
XX
PT Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
PT renal disease, graft versus host disease, and inflammation, comprises
PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide.
XX
PS Example 6; Page 170-172; 175pp; English.
XX
CC A human Fc region polypeptide, which is used in the course of the
CC invention. The specification describes extracellular domains of BR43x2
CC (an isoform of the transmembrane activator and CAML-interactor (TACI)
CC receptor), TACI or BCMA (a related B cell protein). These contain a
CC cysteine rich domain, and are used for inhibiting ztnf4 activity. They
CC may also be used for inhibiting BR43x2, TACI or BCMA receptor-ligand
CC engagement associated with activated or resting B lymphocytes, effector T
CC -cells, or with antibody production. The antibody production is
CC associated with an autoimmune disease selected from systemic lupus
CC erythematosus, myasthenia gravis, multiple sclerosis and rheumatoid
CC arthritis. The ztnf4 activity and BR43x2, TACI or BCMA receptor-ligand
CC engagement is associated with asthma, bronchitis, emphysema, end stage
CC renal failure, glomerulonephritis, vasculitis, nephritis, pyelonephritis,
CC renal neoplasms, multiple myelomas, lymphomas, light chain neuropathy,
CC amyloidosis, moderating immune response, immunosuppression, graft
CC rejection, graft versus host disease, inflammation, insulin dependent
CC diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
CC septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,
CC agonists or antagonists can be used to treat hypertension, renal artery
CC stenosis, or occlusion, and cholesterol or renal emboli
XX
SQ Sequence 251 AA;

Query Match 95.1%; Score 558; DB 3; Length 251;
Best Local Similarity 95.5%; Pred. No. 1.8e-49;
Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              ||   | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         35 APEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 94

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||| ||||||||||||
Db         95 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAK 144
```

Search completed: April 29, 2004, 08:44:21
Job time : 51.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 29, 2004, 08:41:33 ; Search time 13.5 Seconds
(without alignments)
783.783 Million cell updates/sec

Title: US-09-674-857-3
Perfect score: 587
Sequence: 1 APPVAGGPSVFLFPPKPKDT.....CKVSNKGLPSSIEKTISKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	557	94.9	234	2	PT0207	Ig gamma chain C r
2	557	94.9	255	4	S31866	Ig gamma-1 chain C
3	557	94.9	330	1	GHHU	Ig gamma-1 chain C
4	557	94.9	374	2	S69339	Ig heavy chain V r
5	553	94.2	327	1	G4HU	Ig gamma-4 chain C
6	543.5	92.6	326	1	G2HU	Ig gamma-2 chain C
7	539	91.8	377	2	A60764	Ig gamma-3 chain C
8	539	91.8	377	2	A23511	Ig gamma-3 chain C
9	519	88.4	289	1	G3HUWI	Ig gamma-3 heavy c
10	458	78.0	328	2	I47160	Ig gamma 2b chain
11	458	78.0	328	2	I47159	Ig gamma 2a chain
12	453	77.2	277	2	I47162	Ig gamma 4 chain c
13	440	75.0	470	2	S22080	Ig heavy chain pre
14	434	73.9	328	2	I47161	Ig gamma 3 chain c
15	434	73.9	328	2	I47158	Ig gamma 1 chain c
16	431	73.4	333	2	PS0018	Ig gamma-2b chain
17	421	71.7	308	2	C30554	Ig heavy chain C r
18	421	71.7	323	1	GHRB	Ig gamma chain C r
19	421	71.7	329	1	G2GP	Ig gamma-2 chain C
20	421	71.7	472	2	S31459	Ig gamma-1 chain -
21	418	71.2	329	1	G3MSC	Ig gamma-3 chain C
22	418	71.2	398	1	G3MSM	Ig gamma-3 chain C
23	410	69.8	327	2	S06611	Ig gamma-2 chain C
24	397	67.6	405	1	G2MSBM	Ig gamma-2b chain
25	397	67.6	474	1	G2MS11	Ig gamma-2b chain
26	396	67.5	324	1	G1MS	Ig gamma-1 chain C
27	396	67.5	329	2	S00847	Ig gamma-2c chain
28	396	67.5	393	1	G1MSM	Ig gamma-1 chain C
29	396	67.5	444	2	PC4436	monoclonal antibod
30	394	67.1	335	1	G2MSAB	Ig gamma-2a chain
31	391	66.6	330	1	G2MSA	Ig gamma-2a chain
32	391	66.6	399	1	G2MSAM	Ig gamma-2a chain
33	391	66.6	469	2	S37483	Ig gamma-2a chain
34	383	65.2	475	2	S01321	Ig gamma-2b chain
35	381	64.9	446	2	S40295	Ig gamma-2a chain
36	380	64.7	326	2	PS0017	Ig gamma-1 chain C
37	339	57.8	322	2	PS0019	Ig gamma-2a chain
38	309	52.6	112	2	B30503	Ig gamma-2a chain
39	276	47.0	88	2	A30503	Ig gamma-2b chain
40	249	42.4	180	2	I46732	Ig gamma heavy cha
41	167.5	28.5	426	2	I36948	Ig epsilon-chain -
42	166.5	28.4	428	1	EHHU	Ig epsilon chain C
43	162	27.6	152	2	S14236	Ig gamma-1 chain C
44	157	26.7	549	2	S04845	Ig heavy chain pre
45	153	26.1	429	1	EHRT	Ig epsilon chain C

ALIGNMENTS

RESULT 1
PT0207
Ig gamma chain C region - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C;Accession: PT0207
R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A;Reference number: PT0207; MUID:91287716; PMID:2062315
A;Accession: PT0207
A;Molecule type: mRNA
A;Residues: 1-234 <EHR>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;48-117/Domain: immunoglobulin homology <IMM>

Query Match 94.9%; Score 557; DB 2; Length 234;
Best Local Similarity 94.5%; Pred. No. 3.6e-48;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 84

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||| ||: |||||||||
Db         85 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 134
```

RESULT 2
S31866
Ig gamma-1 chain C region - synthetic
C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
R;Filpula, D.
submitted to the EMBL Data Library, February 1993
A;Description: Screeing method for protein-protein interactions of cloned gene products
A;Reference number: S31866
A;Accession: S31866
A;Molecule type: mRNA
A;Residues: 1-255 <FIL>
A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C;Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region

Query Match 94.9%; Score 557; DB 4; Length 255;
Best Local Similarity 94.5%; Pred. No. 4e-48;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         39 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 98

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||| ||: |||||||||
Db         99 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 148


RESULT 3
GHHU
Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432
A;Accession: A93433
A;Molecule type: DNA
A;Residues: 1-330 <ELL>
A;Cross-references: EMBL:Z17370
A;Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,
A;Note: Lys-330 is removed after translation
R;Harris, L.J.
submitted to the EMBL Data Library, October 1992
A;Reference number: S33904
A;Accession: S36861
A;Molecule type: DNA
A;Residues: 2-330 <HAR>
A;Cross-references: EMBL:Z17370
R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A;Reference number: S33887; MUID:83001943; PMID:6811139
A;Accession: S33887
A;Molecule type: DNA
A;Residues: 88-113;235-330 <TAK>
A;Cross-references: EMBL:Z17370
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
A;Reference number: A90563; MUID:71064024; PMID:5489771
A;Contents: myeloma protein Eu
A;Accession: B90563
A;Molecule type: protein
A;Residues: 1-96,'R',98-135 <CUN>
A;Note: this sequence has the G1m(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid seque
A;Reference number: A90564; MUID:71064025; PMID:5530842
A;Contents: Eu
A;Accession: A90564
A;Molecule type: protein
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,
A;Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met
R;Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
igen Primaerstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A;Note: this sequence has the G1m(17) and G1m(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SC
A;Note: this sequence has the G1m(3) and G1m(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfi
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglo
enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             94.9%;  Score 557;  DB 1;  Length 330;
  Best Local Similarity   94.5%;  Pred. No. 5.4e-48;
  Matches  104;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        114 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 173

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||| ||: |||||||||
Db        174 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 223


RESULT 4
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: EMBL:X81695
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology

  Query Match             94.9%;  Score 557;  DB 2;  Length 374;
  Best Local Similarity   94.5%;  Pred. No. 6.2e-48;
```

```
  Matches  104;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 217

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||| ||: |||||||||
Db        218 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 267


RESULT 5
G4HU
Ig gamma-4 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C;Accession: A90933; A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A;Reference number: A90933; MUID:83157104; PMID:6299662
A;Accession: A90933
A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Note: the sequence was determined from the germline gene
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant r
A;Reference number: A90249; MUID:70207560; PMID:4192699
A;Accession: A90249
A;Molecule type: protein
A;Residues: 1-30;81-326 <PIN>
C;Genetics:
A;Gene: GDB:IGHG4
A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;99-110/Region: hinge
F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             94.2%;  Score 553;  DB 1;  Length 327;
  Best Local Similarity   94.5%;  Pred. No. 1.3e-47;
  Matches  104;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              ||   |||||||||||||||||||||||||||||| |||||:|||||||||||||||||
Db        111 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 170

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||:|||||||||||||||||||||||||||||||||||||||||||
Db        171 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 220


RESULT 6
G2HU
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Pudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and
A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A;Note: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constant region domains of a
A;Reference number: A90752; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A;Accession: A90752
A;Molecule type: protein
A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin
A;Reference number: A93132; MUID:80114419; PMID:118920
A;Contents: Zie
A;Accession: A93132
A;Molecule type: protein
A;Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidat
ned
R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG2
A;Cross-references: GDB:119338; OMIM:147110
A;Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;133-202/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,140-200,246-304/Disulfide bonds: #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             92.6%;  Score 543.5;  DB 1;  Length 326;
  Best Local Similarity   92.7%;  Pred. No. 1.2e-46;
  Matches  102;  Conservative    5;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              ||||| |||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        111 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 169

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||:|||:|||||||:|||||||||||||||||: ||||||| |
```

```
Db        170 PREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 219


RESULT 7
A60764
Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

  Query Match             91.8%;  Score 539;  DB 2;  Length 377;
  Best Local Similarity   90.9%;  Pred. No. 3.9e-46;
  Matches  100;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||:| ||||||||||||||
Db        161 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 220

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||:|||||||||||||||||||||||| ||: ||||||| |
Db        221 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 270


RESULT 8
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: co
A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

  Query Match             91.8%;  Score 539;  DB 2;  Length 377;
  Best Local Similarity   90.9%;  Pred. No. 3.9e-46;
  Matches  100;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||:| ||||||||||||||
Db        161 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 220

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||:|||||||||||||||||||||||| ||: ||||||| |
Db        221 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 270


RESULT 9
G3HUWI
Ig gamma-3 heavy chain disease proteins - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C;Accession: A90442; A92219; A90198; A93915; A02149
R;Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy
A;Reference number: A90442; MUID:81021548; PMID:6774747
A;Contents: heavy chain disease protein Wis
A;Accession: A90442
A;Molecule type: protein
A;Residues: 1-289 <FRA>
A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchai
A;Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 c
A;Note: the sequence of residues 42-76 was taken from the reference that follows
R;Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A;Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplicatic
A;Reference number: A92219; MUID:77118561; PMID:402363
A;Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein
A;Accession: A92219
A;Molecule type: protein
A;Residues: 12-97 <MIC>
A;Note: the hinge region in gamma-3 chains is about four times as long as in other gamm
idue segment (12-28)
A;Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inte
R;Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the
A;Reference number: A90198; MUID:77021516; PMID:823945
A;Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues
A;Accession: A90198
A;Molecule type: protein
A;Residues: 59-125,'EB',128-226,228-289 <WOL>
A;Note: this protein lacks most of the V region, all of the CH1 region, and part of the
R;Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A;Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion
A;Reference number: A93915; MUID:82247835; PMID:6808505
A;Contents: heavy chain disease protein Omm
A;Accession: A93915
A;Molecule type: mRNA
A;Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-15
A;Note: a carboxyl-terminal Lys is removed posttranslationally
A;Note: this sequence may represent an allelic form or another gamma chain subclass
C;Comment: The heavy chain disease protein Wis is shown.
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
F;203-270/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             88.4%;  Score 519;  DB 1;  Length 289;
  Best Local Similarity   86.4%;  Pred. No. 2.8e-44;
  Matches   95;  Conservative    9;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||:| ||||||:|||||||
Db         74 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVQVHNAKTK 133

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||:|:|||:|||||||||||:||:|||||||||| ||: ||||||| |
Db        134 PREQQFNSTFRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISKTK 183


RESULT 10
I47160
Ig gamma 2b chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
```

```
C;Accession: I47160
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C;Genetics:
A;Gene: IgG2b
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

  Query Match             78.0%;  Score 458;  DB 2;  Length 328;
  Best Local Similarity   78.8%;  Pred. No. 4.1e-38;
  Matches   82;  Conservative   14;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          7 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 66
              |||||:|||||||||||||||:|||||||| |:|||:|:|||||||| |:|:|:|||:
Db        116 GPSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQF 175

Qy         67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||| : |||||||||:|||:|| ||: | : |||||
Db        176 NSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAK 219


RESULT 11
I47159
Ig gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47159
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C;Genetics:
A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

  Query Match             78.0%;  Score 458;  DB 2;  Length 328;
  Best Local Similarity   78.8%;  Pred. No. 4.1e-38;
  Matches   82;  Conservative   14;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          7 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 66
              |||||:|||||||||||||||:|||||||| |:|||:|:|||||||| |:|:|:|||:
Db        116 GPSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQF 175

Qy         67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||| : |||||||||:|||:|| ||: | : |||||
Db        176 NSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAK 219


RESULT 12
I47162
Ig gamma 4 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47162
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47162
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-277 <KAC>
A;Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
C;Genetics:
A;Gene: IgG4
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>

  Query Match             77.2%;  Score 453;  DB 2;  Length 277;
  Best Local Similarity   77.9%;  Pred. No. 1e-37;
  Matches   81;  Conservative   14;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          7 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 66
              ||| |:|||||||||||||:|||||||| |:|||:|:|||||||| |:|:|:|||:
Db         65 GPSAFIFPPKPKDTLMISRTPKVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQF 124

Qy         67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||| : |||||||||:||||:|| ||: | : |||||
Db        125 NSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAK 168


RESULT 13
S22080
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N;Alternate names: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S22080; S06610; A31303
R;Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A;Reference number: S22080
A;Accession: S22080
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-470 <SAN>
A;Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440
R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gam
A;Reference number: S06610; MUID:90097956; PMID:2513487
A;Accession: S06610
A;Molecule type: DNA
A;Residues: 142-470 <SYM>
A;Cross-references: EMBL:X16701
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Gene: Ig CH gamma-1
A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology <IMM>
F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             75.0%;  Score 440;  DB 2;  Length 470;
  Best Local Similarity   72.5%;  Pred. No. 3.9e-36;
  Matches   79;  Conservative   13;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          2 PPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
              | : ||||||:|||||||||| || |||||||||| |:|||||:|:|| ||||: | |||
Db        253 PELPGGPSVFIFPPKPKDTLTISGTPEVTCVVVDVGHDDPEVKFSWFVDDVEVNTATTKP 312

Qy         62 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||:|||||||| | : ||||  |||:|||| |:|||: | :|||: |
Db        313 REEQFNSTYRVVSALRIQHQDWTGGKEFKCKVHNEGLPAPIVRTISRTK 361


RESULT 14
I47161
Ig gamma 3 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47161
R;Kacskovics, I.; Sun, J.; Butler, J.E.
```

J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47161
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03781; NID:g433127; PIDN:AAA52219.1; PID:g433128
C;Genetics:
A;Gene: IgG3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

  Query Match 73.9%; Score 434; DB 2; Length 328;
  Best Local Similarity 76.7%; Pred. No. 1e-35;
  Matches 79; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

Qy 7 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 66
Db 116 GPSVFIFPPKPKDTLMISQTPEVTCVVVDVSKEHAEVQFSWYVDGVEVHTAETRPKEEQF 175

Qy 67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKA 109
Db 176 NSTYRVVSVLPIQHQDWLKGKEFKCKVNNVDLPAPITRTISKA 218

RESULT 15
I47158
Ig gamma 1 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47158
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47158
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122
C;Genetics:
A;Gene: IgG1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

  Query Match 73.9%; Score 434; DB 2; Length 328;
  Best Local Similarity 76.7%; Pred. No. 1e-35;
  Matches 79; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

Qy 7 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 66
Db 116 GPSVFIFPPKPKDTLMISQTPEVTCVVVDVSKEHAEVQFSWYVDGVEVHTAETRPKEEQF 175

Qy 67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKA 109
Db 176 NSTYRVVSVLPIQHQDWLKGKEFKCKVNNVDLPAPITRTISKA 218

Search completed: April 29, 2004, 08:46:57
Job time : 13.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 29, 2004, 08:37:47 ; Search time 10 Seconds
(without alignments)
572.772 Million cell updates/sec

Title: US-09-674-857-3
Perfect score: 587
Sequence: 1 APPVAGGPSVFLFPPKPKDT.....CKVSNKGLPSSIEKTISKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	557	94.9	330	1	GC1_HUMAN	P01857 homo sapien
2	553	94.2	327	1	GC4_HUMAN	P01861 homo sapien
3	543.5	92.6	326	1	GC2_HUMAN	P01859 homo sapien
4	519	88.4	290	1	GC3_HUMAN	P01860 homo sapien
5	431	73.4	333	1	GCB_RAT	P20761 rattus norv
6	421	71.7	323	1	GC_RABIT	P01870 oryctolagus
7	421	71.7	329	1	GC2_CAVPO	P01862 cavia porce
8	418	71.2	329	1	GC3_MOUSE	P22436 mus musculu
9	418	71.2	398	1	GC3M_MOUSE	P03987 mus musculu
10	397	67.6	336	1	GCB_MOUSE	P01866 mus musculu
11	397	67.6	405	1	GCBM_MOUSE	P01867 mus musculu
12	396	67.5	324	1	GC1_MOUSE	P01868 mus musculu
13	396	67.5	329	1	GCC_RAT	P20762 rattus norv
14	396	67.5	393	1	GC1M_MOUSE	P01869 mus musculu
15	394	67.1	335	1	GCAB_MOUSE	P01864 mus musculu
16	391	66.6	330	1	GCAA_MOUSE	P01863 mus musculu
17	391	66.6	399	1	GCAM_MOUSE	P01865 mus musculu
18	380	64.7	326	1	GC1_RAT	P20759 rattus norv
19	339	57.8	322	1	GCA_RAT	P20760 rattus norv
20	166.5	28.4	428	1	EPC_HUMAN	P01854 homo sapien
21	153	26.1	429	1	EPC_RAT	P01855 rattus norv
22	153	26.1	457	1	MUC_SUNMU	P20768 suncus muri
23	138	23.5	421	1	EPC_MOUSE	P06336 mus musculu
24	138	23.5	454	1	MUC_HUMAN	P01871 homo sapien
25	137.5	23.4	299	1	ALC_RABIT	P01879 oryctolagus
26	136	23.2	391	1	MUCB_HUMAN	P04220 homo sapien
27	132	22.5	454	1	MUC_MESAU	P06337 mesocricetu
28	132	22.5	455	1	MUC_MOUSE	P01872 mus musculu
29	132	22.5	476	1	MUCM_MOUSE	P01873 mus musculu
30	131	22.3	106	1	KAC_HUMAN	P01834 homo sapien
31	130	22.1	103	1	LAC_CHICK	P20763 gallus gall
32	125	21.3	450	1	MUC_CANFA	P01874 canis famil
33	121.5	20.7	105	1	LAC1_MOUSE	P01843 mus musculu
34	121.5	20.7	105	1	LAC5_MUSSP	P20765 mus spretus
35	120	20.4	458	1	MUC_RABIT	P03988 oryctolagus
36	120	20.4	479	1	MUCM_RABIT	P04221 oryctolagus
37	119.5	20.4	340	1	ALC2_HUMAN	P01877 homo sapien
38	119.5	20.4	353	1	ALC1_GORGO	P20758 gorilla gor
39	119.5	20.4	353	1	ALC1_HUMAN	P01876 homo sapien
40	117.5	20.0	105	1	LAC5_MOUSE	P20764 mus musculu
41	112	19.1	103	1	KAC4_RABIT	P01840 oryctolagus
42	111.5	19.0	344	1	ALC_MOUSE	P01878 mus musculu
43	111.5	19.0	393	1	HVC3_HETFR	P23086 heterodontu
44	110.5	18.8	213	1	ILL1_HUMAN	P15814 homo sapien
45	109.5	18.7	105	1	LAC_HUMAN	P01842 homo sapien

ALIGNMENTS

RESULT 1
GC1_HUMAN
ID GC1_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ig gamma-1 chain C region.
GN IGHG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gammal gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [3]
RP SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL Biochemistry 9:3171-3181(1970).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=77070269; PubMed=826475;
RA Ponstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a
RT monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The
RT chymotryptic peptides of the H-chain, alignment of the tryptic
RT peptides and discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [5]
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.

```
RT   Intrachain disulfide bonds.";
RL   Biochemistry 9:3188-3196(1970).
RN   [7]
RP   DISULFIDE BONDS.
RX   MEDLINE=77070267; PubMed=1002129;
RA   Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
RT   characterization of the protein, the L- and H-chains, the
RT   cyanogen bromide cleavage products, and the disulfide bridges.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX   MEDLINE=81208100; PubMed=7236608;
RA   Deisenhofer J.;
RT   "Crystallographic refinement and atomic models of a human Fc fragment
RT   and its complex with fragment B of protein A from Staphylococcus
RT   aureus at 2.9- and 2.8-A resolution.";
RL   Biochemistry 20:2361-2370(1981).
CC   -!- MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and the
CC       G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the
CC       G1M(3) marker and the G1M (non-1) markers.
CC   -!- MISCELLANEOUS: Nie also differs in the amidation states of
CC       35, 116, 198, 269 and 272.
CC   -!- MISCELLANEOUS: EU also differs in the amidation states of residues
CC       155, 166, 177, 195, 198, 269, and 272 and in the order of residues
CC       268-272.
CC   -!- MISCELLANEOUS: KOL also differs in the amidation states of
CC       residues 198, 267 and 272.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00228; AAC82527.1; ALT_INIT.
DR   PIR; A93433; GHHU.
DR   PDB; 1FC1; 15-JUL-92.
DR   PDB; 1FC2; 15-JUL-92.
DR   PDB; 1AJ7; 12-NOV-97.
DR   PDB; 1D5B; 09-FEB-00.
DR   PDB; 1D5I; 09-FEB-00.
DR   PDB; 1D6V; 04-OCT-00.
DR   PDB; 1DN2; 17-MAY-00.
DR   PDB; 1E4K; 06-JUN-01.
DR   PDB; 1FCC; 20-JUL-95.
DR   PDB; 1HZH; 12-JUN-02.
DR   PDB; 1I7Z; 08-AUG-01.
DR   PDB; 1IIS; 16-MAY-01.
DR   PDB; 1IIX; 16-MAY-01.
DR   PDB; 1L6X; 10-APR-02.
DR   PDB; 2RCS; 12-NOV-97.
DR   Genew; HGNC:5525; IGHG1.
DR   MIM; 147100; -.
DR   GO; GO:0005624; C:membrane fraction; NAS.
DR   GO; GO:0003823; F:antigen binding; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   3D-structure.
FT   NON_TER       1      1
FT   DOMAIN        1     98       CH1.
FT   DOMAIN       99    110       HINGE.
FT   DOMAIN      111    223       CH2.
FT   DOMAIN      224    330       CH3.
FT   DISULFID     27     83
FT   DISULFID    103    103       INTERCHAIN (WITH LIGHT CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH HEAVY CHAIN).
FT   DISULFID    112    112       INTERCHAIN (WITH HEAVY CHAIN).
FT   DISULFID    144    204
FT   DISULFID    250    308
FT   CARBOHYD    180    180       N-LINKED (GLCNAC. . .).
FT   MOD_RES     330    330       REMOVED POST-TRANSLATIONALLY.
FT   VARIANT      97     97       K -> R (IN G1M(3) MARKER).
FT                                /FTId=VAR_003886.
FT   VARIANT     239    239       D -> E (IN G1M(NON-1) MARKER).
FT                                /FTId=VAR_003887.
FT   VARIANT     241    241       L -> M (IN G1M(NON-1) MARKER).
FT                                /FTId=VAR_003888.
FT   STRAND      122    126
FT   HELIX       130    134
FT   TURN        136    137
FT   STRAND      141    147
FT   STRAND      157    162
FT   TURN        163    164
FT   STRAND      165    166
FT   TURN        168    171
FT   STRAND      176    179
FT   TURN        180    181
FT   STRAND      182    190
FT   HELIX       193    197
FT   TURN        198    199
FT   STRAND      202    207
FT   TURN        209    210
FT   STRAND      215    219
FT   STRAND      227    227
FT   STRAND      230    234
FT   HELIX       238    242
FT   STRAND      245    256
FT   STRAND      260    265
FT   STRAND      270    270
FT   STRAND      274    276
FT   STRAND      280    281
FT   TURN        283    284
FT   STRAND      287    296
FT   HELIX       297    301
FT   TURN        302    303
FT   STRAND      305    312
FT   TURN        313    314
FT   TURN        316    317
FT   STRAND      320    325
SQ   SEQUENCE   330 AA;  36106 MW;  3770EE106C2FA33D CRC64;

  Query Match             94.9%;  Score 557;  DB 1;  Length 330;
  Best Local Similarity   94.5%;  Pred. No. 5.2e-49;
  Matches  104;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        114 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 173

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||| ||: |||||||||
Db        174 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 223


RESULT 2
GC4_HUMAN
ID   GC4_HUMAN      STANDARD;      PRT;   327 AA.
AC   P01861;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig gamma-4 chain C region.
GN   IGHG4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83157104; PubMed=6299662;
RA   Ellison J.W., Buxbaum J.N., Hood L.E.;
RT   "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL   DNA 1:11-18(1981).
RN   [2]
RP   SEQUENCE OF 1-30 AND 81-326.
RX   MEDLINE=70207560; PubMed=4192699;
RA   Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT   "Human immunoglobulin subclasses. Partial amino acid sequence of the
RT   constant region of a gamma 4 chain.";
RL   Biochem. J. 117:33-47(1970).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; K01316; AAB59394.1; ALT_INIT.
DR   PIR; A90933; G4HU.
DR   PDB; 1ADQ; 16-SEP-98.
DR   Genew; HGNC:5528; IGHG4.
DR   MIM; 147130; -.
DR   GO; GO:0005624; C:membrane fraction; NAS.
DR   GO; GO:0003823; F:antigen binding; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT   NON_TER       1      1
FT   DOMAIN        1     98       CH1.
FT   DOMAIN       99    110       HINGE.
FT   DOMAIN      111    220       CH2.
FT   DOMAIN      221    327       CH3.
FT   DISULFID     14     14       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     83
FT   DISULFID    106    106       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    141    201
FT   DISULFID    247    305
SQ   SEQUENCE   327 AA;  35940 MW;  3EDBD811EF208E7A CRC64;

  Query Match             94.2%;  Score 553;  DB 1;  Length 327;
  Best Local Similarity   94.5%;  Pred. No. 1.3e-48;
  Matches  104;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              ||   |||||||||||||||||||||||||||||||| |||||:|||||||||||||||||
Db        111 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 170

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||:|||||||||||||||||||||||||||||||||||||||||||||
Db        171 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 220


RESULT 3
GC2_HUMAN
ID   GC2_HUMAN      STANDARD;      PRT;   326 AA.
AC   P01859;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig gamma-2 chain C region.
GN   IGHG2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE OF 2-326 FROM N.A.
RX   MEDLINE=82197621; PubMed=6804948;
RA   Ellison J.W., Hood L.E.;
RT   "Linkage and sequence homology of two human immunoglobulin gamma
RT   heavy chain constant region genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN   [2]
RP   SEQUENCE OF 88-115 FROM N.A.
RC   TISSUE=Fetal liver;
RX   MEDLINE=83001943; PubMed=6811139;
RA   Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
RT   "Structure of human immunoglobulin gamma genes: implications for
RT   evolution of a gene family.";
RL   Cell 29:671-679(1982).
RN   [3]
RP   SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RC   TISSUE=Fetal liver;
RX   MEDLINE=84235992; PubMed=6329676;
RA   Krawinkel U., Rabbitts T.H.;
RT   "Comparison of the hinge-coding segments in human immunoglobulin gamma
RT   heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
RT   genes.";
RL   EMBO J. 1:403-407(1982).
RN   [4]
RP   SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX   MEDLINE=81007873; PubMed=6774012;
RA   Wang A.-C., Tung E., Fudenberg H.H.;
RT   "The primary structure of a human IgG2 heavy chain: genetic,
RT   evolutionary, and functional implications.";
RL   J. Immunol. 125:1048-1054(1980).
RN   [5]
RP   SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX   MEDLINE=80001357; PubMed=113060;
RA   Connell G.E., Parr D.M., Hofmann T.;
RT   "The amino acid sequences of the three heavy chain constant region
RT   domains of a human IgG2 myeloma protein.";
RL   Can. J. Biochem. 57:758-767(1979).
RN   [6]
RP   SEQUENCE OF 238-275 (ZIE).
RX   MEDLINE=80114419; PubMed=118920;
RA   Hofmann T., Parr D.M.;
RT   "A note of the amino acid sequence of residues 381-391 of human
RT   immunoglobulins gamma chains.";
RL   Mol. Immunol. 16:923-925(1979).
RN   [7]
RP   REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RA   Hofmann T., Parr D.M.;
RL   Submitted (MAR-1980) to the PIR data bank.
RN   [8]
RP   SEQUENCE OF 1-121 (DOT).
RX   MEDLINE=95255298; PubMed=7737190;
RA   Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT   "Characterization of the two unique human anti-flavin monoclonal
RT   immunoglobulins.";
RL   Eur. J. Biochem. 228:886-893(1995).
RN   [9]
RP   DISULFIDE BONDS.
RX   MEDLINE=72033500; PubMed=4940472;
RA   Milstein C., Frangione B.;
RT   "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RL   Biochem. J. 121:217-225(1971).
RN   [10]
RP   DISULFIDE BONDS.
RX   MEDLINE=69064124; PubMed=5782707;
RA   Frangione B., Milstein C., Pink J.R.L.;
RT   "Structural studies of immunoglobulin G.";
```

```
RL   Nature 221:145-148(1969).
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; J00230; AAB59393.1; -.
DR   PIR; A93906; G2HU.
DR   HSSP; P01857; 1FC1.
DR   Genew; HGNC:5526; IGHG2.
DR   MIM; 147110; -.
DR   GO; GO:0005624; C:membrane fraction; NAS.
DR   GO; GO:0003823; F:antigen binding; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Immunoglobulin domain; Immunoglobulin C region.
FT   NON_TER       1      1
FT   DOMAIN        1     98       CH1.
FT   DOMAIN       99    110       HINGE.
FT   DOMAIN      111    219       CH2.
FT   DOMAIN      220    326       CH3.
FT   DISULFID     14     14       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     83
FT   DISULFID    102    102       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    103    103       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    106    106       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    140    200
FT   DISULFID    246    304
FT   SITE        156    156       AT OR NEAR THE COMPLEMENT-BINDING SITE.
FT   MOD_RES     326    326       REMOVED POST-TRANSLATIONALLY (PROBABLE).
FT   VARIANT      60     60       S -> A (IN MYELOMA PROTEINS TIL & ZIE).
FT                                /FTId=VAR_003889.
FT   CONFLICT    109    109       C -> S (IN REF. 3).
SQ   SEQUENCE   326 AA;  35884 MW;  8310878C6878CF9C CRC64;

  Query Match             92.6%;  Score 543.5;  DB 1;  Length 326;
  Best Local Similarity   92.7%;  Pred. No. 1.2e-47;
  Matches  102;  Conservative    5;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              ||||| |||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db        111 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 169

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAX 110
              |||||:|||:||||||||:||||||||||||||||||||: ||||||| |
Db        170 PREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTX 219


RESULT 4
GC3_HUMAN
ID   GC3_HUMAN      STANDARD;      PRT;   290 AA.
AC   P01860;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
GN   IGHG3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE (DISEASE PROTEIN WIS).
RX   MEDLINE=81021548; PubMed=6774747;
RA   Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
RT   "Primary structure of human gamma 3 immunoglobulin deletion mutant:
RT   gamma 3 heavy-chain disease protein Wis.";
RL   Biochemistry 19:4304-4308(1980).
RN   [2]
RP   REVISIONS TO 12-97 (PROTEIN WIS).
RX   MEDLINE=77118561; PubMed=402363;
RA   Michaelsen T.E., Frangione B., Franklin E.C.;
RT   "Primary structure of the 'hinge' region of human IgG3. Probable
RT   quadruplication of a 15-amino acid residue basic unit.";
RL   J. Biol. Chem. 252:883-889(1977).
RN   [3]
RP   REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).
RX   MEDLINE=77021516; PubMed=823945;
RA   Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
RT   "The amino acid sequence of 'heavy chain disease' protein ZUC.
RT   Structure of the Fc fragment of immunoglobulin G3.";
RL   Biochem. Biophys. Res. Commun. 71:907-914(1976).
RN   [4]
RP   SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RX   MEDLINE=82247835; PubMed=6808505;
RA   Alexander A., Steinmetz M., Barritault D., Frangione B.,
RA   Franklin E.C., Hood L., Buxbaum J.N.;
RT   "Gamma Heavy chain disease in man: cDNA sequence supports partial
RT   gene deletion model.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
CC   -!- SUBUNIT: Dimer linked by 12 disulfide bonds; it has an extra
CC       interchain disulfide bond at position 7 in addition to the 11
CC       normally present in the hinge region.
CC   -!- MISCELLANEOUS: The heavy chain disease protein WIS is shown.
CC   -!- MISCELLANEOUS: The sequence of residues 42-76 was taken from the
CC       Ref.2.
CC   -!- MISCELLANEOUS: Disease protein WIS is lacking most of the V region
CC       and all of the CH1 region.
CC   -!- MISCELLANEOUS: Disease protein ZUC lack most of the V region, all
CC       of the CH1 region, and part of the hinge compared with normal
CC       gamma-3 heavy chains.
CC   -!- MISCELLANEOUS: Disease protein OMM may represent an allelic form
CC       or another gamma chain subclass.
CC   -!- MISCELLANEOUS: The hinge region in gamma-3 chains is about four
CC       times as long as in other gamma chains and contains three
CC       identical 15-residue segments preceded by a similar 17-residue
CC       segment (12-28).
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; J00231; AAA52805.1; ALT_SEQ.
DR   HSSP; P01857; 1FC1.
DR   Genew; HGNC:5527; IGHG3.
DR   MIM; 147120; -.
DR   GO; GO:0005624; C:membrane fraction; NAS.
DR   GO; GO:0003823; F:antigen binding; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat;
KW   Pyrrolidone carboxylic acid.
FT   DOMAIN       12     73       HINGE.
FT   DOMAIN       74    183       CH2.
FT   DOMAIN      184    289       CH3.
```

```
FT   REPEAT       29     43
FT   REPEAT       44     58
FT   REPEAT       59     73
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   CARBOHYD      6      6       N-LINKED (GLCNAC. . .).
FT   DISULFID      7      7       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     24     24       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     27     27       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     33     33       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     39     39       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     42     42       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     48     48       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     54     54       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     57     57       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     63     63       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     69     69       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     72     72       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   CARBOHYD    140    140       N-LINKED (GLCNAC. . .).
FT   MOD_RES     290    290       REMOVED POST-TRANSLATIONALLY.
FT   VARIANT     126    127       QV -> EB (IN ZUC).
FT                                /FTId=VAR_003890.
FT   VARIANT     134    134       P -> L (IN OMM).
FT                                /FTId=VAR_003891.
FT   VARIANT     139    139       F -> Y (IN OMM).
FT                                /FTId=VAR_003892.
FT   VARIANT     182    182       T -> A (IN OMM).
FT                                /FTId=VAR_003893.
FT   VARIANT     227    227       S -> N (IN OMM).
FT                                /FTId=VAR_003894.
FT   VARIANT     227    227       MISSING (IN ZUC).
FT                                /FTId=VAR_003895.
FT   VARIANT     279    279       F -> Y (IN OMM).
FT                                /FTId=VAR_003896.
SQ   SEQUENCE   290 AA;  32331 MW;  E69CBC95705B2F46 CRC64;

  Query Match             88.4%;  Score 519;  DB 1;  Length 290;
  Best Local Similarity   86.4%;  Pred. No. 3.1e-45;
  Matches   95;  Conservative    9;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||:| ||||||:|||||||
Db         74 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVQVHNAKTK 133

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||:|:|||:|||||||||||:||:||||||||||| ||: ||||||| |
Db        134 PREQQFNSTFRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISKTK 183


RESULT 5
GCB_RAT
ID   GCB_RAT        STANDARD;      PRT;   333 AA.
AC   P20761;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig gamma-2B chain C region.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89232738; PubMed=3149946;
RA   Brueggemann M.;
RT   "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL   Gene 74:473-482(1988).
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
DR   PIR; PS0018; PS0018.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Repeat.
FT   NON_TER       1      1
FT   DOMAIN        6     96       IG-LIKE 1.
FT   DOMAIN      124    223       IG-LIKE 2.
FT   DOMAIN      232    328       IG-LIKE 3.
FT   DISULFID     15     15       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     80
FT   DISULFID    106    106       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    112    112       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    115    115       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    147    207
FT   DISULFID    253    311
SQ   SEQUENCE   333 AA;  36497 MW;  55F8B64D48D460A6 CRC64;

  Query Match             73.4%;  Score 431;  DB 1;  Length 333;
  Best Local Similarity   69.7%;  Pred. No. 2.9e-36;
  Matches   76;  Conservative   19;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          2 PPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
              | : |||||:|||||||  |:||:  :|||||||||  |:|:|:|:|:|:  |||  |:|:|
Db        118 PELLGGPSVFIFPPKPKDILLISQNAKVTCVVVDVSEEEPDVQFSWFVNNVEVHTAQTQP 177

Qy         62 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||:|||| | : ||||::|||:||||:|| ||| |||||||| |
Db        178 REEQYNSTFRVVSALPIQHQDWMSGKEFKCKVNNKALPSPIEKTISKPK 226


RESULT 6
GC_RABIT
ID   GC_RABIT       STANDARD;      PRT;   323 AA.
AC   P01870;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig gamma chain C region.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84030930; PubMed=6313520;
RA   Bernstein K.E., Alexander C.B., Mage R.G.;
RT   "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
RT   F-I haplotype.";
RL   Immunogenetics 18:387-397(1983).
RN   [2]
RP   SEQUENCE OF 1-128.
RX   MEDLINE=76135469; PubMed=1243651;
RA   Pratt D.M., Mole L.E.;
RT   "Sequence studies on the constant region of the Fd sections of rabbit
RT   immunoglobulin G of different allotype.";
RL   Biochem. J. 151:337-349(1975).
RN   [3]
RP   SEQUENCE OF 88-266 FROM N.A.
RX   MEDLINE=83299917; PubMed=6193512;
RA   Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT   "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
RT   heavy chain and identification of two genomic C gamma genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN   [4]
RP   SEQUENCE OF 132-161.
RX   MEDLINE=70110015; PubMed=5461106;
RA   Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT   "Sequence studies of the Fd section of the heavy chain of rabbit
RT   immunoglobulin G.";
RL   Biochem. J. 116:249-259(1970).
RN   [5]
RP   SEQUENCE OF 129-131 AND 155-322.
```

```
RA   Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
RL   (In) Killander J. (eds.);
RL   Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
RL   Stockholm (1967).
CC   -!- MISCELLANEOUS: Ref.1 sequence has the D12 allotypic marker,
CC       104-Thr, and the E14 marker, 185-Thr. Ref.3 has the D11 and E15
CC       markers and Ref.5 the E15 marker.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M16426; AAA31289.1; -.
DR   PIR; A91749; GHRB.
DR   HSSP; P01857; 1FC1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Repeat.
FT   NON_TER       1      1
FT   DOMAIN        6     96       IG-LIKE 1.
FT   DOMAIN      114    213       IG-LIKE 2.
FT   DOMAIN      222    318       IG-LIKE 3.
FT   VARIANT     104    104       T -> M (IN D11 MARKER).
FT   VARIANT     185    185       T -> A (IN E15 MARKER).
FT   CONFLICT     48     48       N -> E (IN REF. 2).
FT   CONFLICT     71     71       V -> VPV (IN REF. 2).
FT   CONFLICT    144    144       Q -> E (IN REF. 3 AND 4).
FT   CONFLICT    173    173       N -> D (IN REF. 5).
FT   CONFLICT    187    187       Q -> E (IN REF. 3 AND 5).
FT   CONFLICT    201    201       N -> D (IN REF. 5).
FT   CONFLICT    218    218       Q -> E (IN REF. 5).
FT   CONFLICT    233    233       E -> Q (IN REF. 5).
FT   CONFLICT    246    246       N -> D (IN REF. 5).
FT   CONFLICT    256    256       E -> G (IN REF. 5).
FT   CONFLICT    260    260       N -> D (IN REF. 5).
FT   CONFLICT    266    266       N -> D (IN REF. 5).
FT   CONFLICT    280    280       Y -> W (IN REF. 5).
FT   CONFLICT    284    284       N -> S (IN REF. 5).
SQ   SEQUENCE   323 AA;  35404 MW;  69E8AA118D579A8B CRC64;

  Query Match             71.7%;  Score 421;  DB 1;  Length 323;
  Best Local Similarity   69.7%;  Pred. No. 2.9e-35;
  Matches   76;  Conservative   14;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          2 PPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
              | : ||||||:|||||||||||||||||||||||||| :||||:| ||::  :|  |:
Db        108 PELLGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTARPPL 167

Qy         62 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||:|:||| |||| | : ||||| |||:|||| || ||: |||||||:
Db        168 REQQFNSTIRVVSTLPITHQDWLRGKEFKCKVHNKALPAPIEKTISKAR 216


RESULT 7
GC2_CAVPO
ID   GC2_CAVPO      STANDARD;      PRT;   329 AA.
AC   P01862;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig gamma-2 chain C region.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE OF 1-3.
RA   Trischmann T.M.;
RL   Submitted (APR-1975) to the PIR data bank.
RN   [2]
RP   SEQUENCE OF 4-68.
RX   MEDLINE=71058471; PubMed=5538606;
RA   Birshtein B.K., Hussain Q.Z., Cebra J.J.;
RT   "Structure of heavy chain from strain 13 guinea pig
RT   immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT   half-cystine joining heavy and light chains.";
RL   Biochemistry 10:18-25(1971).
RN   [3]
RP   SEQUENCE OF 69-133 AND 312-329.
RX   MEDLINE=71058486; PubMed=5538616;
RA   Turner K.J., Cebra J.J.;
RT   "Structure of heavy chain from strain 13 guinea pig
RT   immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT   and hinge region cyanogen bromide fragments.";
RL   Biochemistry 10:9-17(1971).
RN   [4]
RP   SEQUENCE OF 134-226.
RX   MEDLINE=75036072; PubMed=4429665;
RA   Tracey D.E., Cebra J.J.;
RT   "Primary structure of the CH2 homology region from guinea pig IgG2
RT   antibodies.";
RL   Biochemistry 13:4796-4803(1974).
RN   [5]
RP   SEQUENCE OF 227-311.
RX   MEDLINE=75036073; PubMed=4609467;
RA   Trischmann T.M., Cebra J.J.;
RT   "Primary structure of the CH3 homology region from guinea pig IgG2
RT   antibodies.";
RL   Biochemistry 13:4804-4811(1974).
RN   [6]
RP   DISULFIDE BONDS.
RX   MEDLINE=71058474; PubMed=4922544;
RA   Oliveira B., Lamm M.E.;
RT   "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL   Biochemistry 10:26-31(1971).
CC   -!- MISCELLANEOUS: This chain was isolated from pooled serum of strain
CC       13 inbred guinea pigs.
DR   PIR; A94553; G2GP.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT   NON_TER       1      1
FT   DISULFID     16     16       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     28     79
FT   DISULFID    105    105       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    107    107       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    110    110       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    142    202
FT   CARBOHYD    178    178       N-LINKED (GLCNAC. . .).
FT   DISULFID    248    308
SQ   SEQUENCE   329 AA;  36074 MW;  5D231B7164D1FBA9 CRC64;

  Query Match             71.7%;  Score 421;  DB 1;  Length 329;
  Best Local Similarity   71.6%;  Pred. No. 2.9e-35;
  Matches   78;  Conservative   11;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 PPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
              |  ||||||:|||||||||||| || ||||||||| ::|||:| |:||   | ||:|||
Db        113 PENLGGPSVFIFPPKPKDTLMISLTPRVTCVVVDVSQDEPEVQFTWFVDNKPVGNAETKP 172
```

```
Qy          62 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
               | ||||:|:|| ||| : ||||| |||:|||| || ||: ||||||| |
Db         173 RVEQYNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKTK 221


RESULT 8
GC3_MOUSE
ID   GC3_MOUSE      STANDARD;      PRT;   329 AA.
AC   P22436;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig gamma-3 chain C region, secreted form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85027161; PubMed=6092053;
RA   Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA   Tucker P.W., Blattner F.R.;
RT   "Structural analysis of the murine IgG3 constant region gene.";
RL   EMBO J. 3:2041-2046(1984).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00451; -; NOT_ANNOTATED_CDS.
DR   PIR; B02156; G3MSC.
DR   HSSP; P01857; 1FC1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Transmembrane; Alternative splicing.
FT   NON_TER       1      1
FT   DOMAIN        1     97       CH1.
FT   DOMAIN       98    113       HINGE.
FT   DOMAIN      114    223       CH2.
FT   DOMAIN      224    327       CH3.
SQ   SEQUENCE   329 AA;  36228 MW;  F45827174182BAD6 CRC64;

  Query Match             71.2%;  Score 418;  DB 1;  Length 329;
  Best Local Similarity   68.5%;  Pred. No. 5.9e-35;
  Matches   76;  Conservative   15;  Mismatches   18;  Indels    2;  Gaps    1;

Qy           2 PP--VAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 59
               ||  : |||||||:||||||| |||| ||:||||||||| :||:|  :|:||  ||| | |
Db         112 PPGNILGGPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWT 171

Qy          60 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
               :||| |||||:|||| | : ||||: |||:||||:|| ||: ||:|||| |
Db         172 QPREAQYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPK 222


RESULT 9
GC3M_MOUSE
ID   GC3M_MOUSE     STANDARD;      PRT;   398 AA.
AC   P03987;
DT   23-OCT-1986 (Rel. 02, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig gamma-3 chain C region, membrane-bound form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85027161; PubMed=6092053;
RA   Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA   Tucker P.W., Blattner F.R.;
RT   "Structural analysis of the murine IgG3 constant region gene.";
RL   EMBO J. 3:2041-2046(1984).
RN   [2]
RP   SEQUENCE OF 328-398 FROM N.A.
RX   MEDLINE=84041483; PubMed=6314258;
RA   Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA   Wall R.;
RT   "The structure of the mouse immunoglobulin in gamma 3 membrane gene
RT   segment.";
RL   Nucleic Acids Res. 11:6775-6785(1983).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00451; AAB59655.1; -.
DR   EMBL; V01526; CAA24767.1; ALT_SEQ.
DR   PIR; A02156; G3MSM.
DR   HSSP; P01857; 1FC1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Transmembrane; Alternative splicing.
FT   NON_TER       1      1
FT   DOMAIN        1     97       CH1.
FT   DOMAIN       98    113       HINGE.
FT   DOMAIN      114    223       CH2.
FT   DOMAIN      224    327       CH3.
FT   TRANSMEM    346    362       POTENTIAL.
FT   DOMAIN      363    398       CYTOPLASMIC (POTENTIAL).
FT   CONFLICT    333    333       E -> G (IN REF. 2).
FT   CONFLICT    342    342       E -> Q (IN REF. 2).
FT   CONFLICT    388    388       P -> F (IN REF. 2).
SQ   SEQUENCE   398 AA;  43929 MW;  CF7F264B50A41B95 CRC64;

  Query Match             71.2%;  Score 418;  DB 1;  Length 398;
  Best Local Similarity   68.5%;  Pred. No. 7.3e-35;
  Matches   76;  Conservative   15;  Mismatches   18;  Indels    2;  Gaps    1;

Qy           2 PP--VAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 59
               ||  : |||||||:||||||| |||| ||:||||||||| :||:|  :|:||  ||| | |
Db         112 PPGNILGGPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWT 171

Qy          60 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
               :||| |||||:|||| | : ||||: |||:||||:|| ||: ||:|||| |
Db         172 QPREAQYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPK 222


RESULT 10
GCB_MOUSE
ID   GCB_MOUSE      STANDARD;      PRT;   336 AA.
AC   P01866;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
```

```
DE   Ig gamma-2B chain C region secreted form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ALLELE A).
RX   MEDLINE=80120716; PubMed=6766534;
RA   Yamawaki-Kataoka Y., Kataoka T., Takahashi N., Obata M., Honjo T.;
RT   "Complete nucleotide sequence of immunoglobulin gamma2b chain gene
RT   cloned from newborn nouse DNA.";
RL   Nature 283:786-789(1980).
RN   [2]
RP   SEQUENCE FROM N.A. (MPC 11).
RX   MEDLINE=80081501; PubMed=117548;
RA   Tucker P.W., Marcu K.B., Slightom J.L., Blattner F.R.;
RT   "Structure of the constant and 3' untranslated regions of the murine
RT   gamma 2b heavy chain messenger RNA.";
RL   Science 206:1299-1303(1979).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=80081502; PubMed=117549;
RA   Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R.;
RT   "Sequence of the cloned gene for the constant region of murine gamma
RT   2b immunoglobulin heavy chain.";
RL   Science 206:1303-1306(1979).
RN   [4]
RP   SEQUENCE FROM N.A. (ALLELE B).
RX   MEDLINE=82173203; PubMed=6803173;
RA   Ollo R., Rougeon F.;
RT   "Mouse immunoglobulin allotypes: post-duplication divergence of gamma
RT   2a and gamma 2b chain genes.";
RL   Nature 296:761-763(1982).
RN   [5]
RP   CARBOHYDRATE-LINKAGE SITE THR-105.
RX   MEDLINE=94216359; PubMed=7512967;
RA   Kim H., Yamaguchi Y., Masuda K., Matsunaga C., Yamamoto K.,
RA   Irimura T., Takahashi N., Kato K., Arata Y.;
RT   "O-glycosylation in hinge region of mouse immunoglobulin G2b.";
RL   J. Biol. Chem. 269:12345-12350(1994).
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Secreted;
CC         IsoId=P01866-1; Sequence=Displayed;
CC         Note=May be the major isoform;
CC       Name=Membrane-bound;
CC         IsoId=P01867-1; Sequence=External;
CC   -!- PTM: O-LINKED GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH IS
CC       MODIFIED WITH 2 SIALIC ACID RESIDUES.
CC   -!- PTM: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA CHAINS.
CC   -!- MISCELLANEOUS: The a allele sequence is shown.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
DR   PIR; S25057; G2MS11.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Alternative splicing; Repeat.
FT   NON_TER       1      1
FT   DOMAIN        6     98       IG-LIKE 1.
FT   DOMAIN      127    226       IG-LIKE 2.
FT   DOMAIN      235    331       IG-LIKE 3.
FT   DISULFID     15     15       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     82
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    112    112       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    115    115       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    118    118       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    150    210
FT   DISULFID    256    314
FT   CARBOHYD    105    105       O-LINKED (GALNAC. . .).
FT   MOD_RES     336    336       REMOVED POST-TRANSLATIONALLY (PROBABLE).
FT   VARIANT     163    163       Q -> R (IN ALLELE B).
FT   VARIANT     194    194       T -> A (IN ALLELE B).
FT   VARIANT     300    300       N -> D (IN ALLELE B).
FT   VARIANT     301    301       M -> I (IN ALLELE B).
FT   CONFLICT     25     25       L -> S (IN REF. 2 AND 3).
FT   CONFLICT     36     36       S -> P (IN REF. 2 AND 3).
FT   CONFLICT    239    239       I -> T (IN REF. 2 AND 3).
SQ   SEQUENCE   336 AA;  36658 MW;  7D879662607C356E CRC64;

  Query Match             67.6%;  Score 397;  DB 1;  Length 336;
  Best Local Similarity   65.5%;  Pred. No. 8e-33;
  Matches   72;  Conservative   17;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||:|||  || |||| ||:|||||||| :||:|: :|:|: |||| |:|:
Db        120 APNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQ 179

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                | |||| |||| | : ||||::|||:||||:|| ||| ||:|||| |
Db        180 THREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIK 229


RESULT 11
GCBM_MOUSE
ID   GCBM_MOUSE     STANDARD;      PRT;   405 AA.
AC   P01867;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ig gamma-2B chain C region, membrane-bound form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE OF 335-405 FROM N.A.
RX   MEDLINE=82222190; PubMed=6283537;
RA   Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT   "Nucleotide sequences of gene segments encoding membrane domains of
RT   immunoglobulin gamma chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
RN   [2]
RP   SEQUENCE OF 335-378 FROM N.A.
RX   MEDLINE=82115295; PubMed=6799207;
RA   Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA   Eisenberg D., Wall R.;
RT   "Gene segments encoding transmembrane carboxyl termini of
RT   immunoglobulin gamma chains.";
RL   Cell 26:19-27(1981).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Membrane-bound;
CC         IsoId=P01867-1; Sequence=Displayed;
CC       Name=Secreted;
CC         IsoId=P01866-1; Sequence=External;
CC         Note=May be the major isoform;
CC   -!- PTM: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA CHAINS.
CC   -!- MISCELLANEOUS: The sequence of residues 1-335 is assumed to be
CC       identical with the corresponding region of the secreted form.
CC   -!- MISCELLANEOUS: The a allele sequence is shown.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
```

```
CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; J00462; AAB59659.1; ALT_INIT.
DR   PIR; C02154; G2MSBM.
DR   PDB; 1CIC; 11-MAR-03.
DR   MGD; MGI:96445; Igh-3.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Transmembrane;
KW   Alternative splicing; 3D-structure; Repeat.
FT   NON_TER       1      1
FT   DOMAIN        6     98       IG-LIKE 1.
FT   DOMAIN      127    226       IG-LIKE 2.
FT   DOMAIN      235    331       IG-LIKE 3.
FT   DISULFID     15     15       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     82
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    112    112       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    115    115       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    118    118       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    150    210
FT   DISULFID    256    314
FT   TRANSMEM    352    369       POTENTIAL.
FT   DOMAIN      370    405       CYTOPLASMIC (POTENTIAL).
SQ   SEQUENCE   405 AA;  44330 MW;  89B3CF0A9B6D49FA CRC64;

  Query Match             67.6%;  Score 397;  DB 1;  Length 405;
  Best Local Similarity   65.5%;  Pred. No. 9.9e-33;
  Matches   72;  Conservative   17;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||:|||  || |||| ||:||||||||| :||:|: :|:|: |||| |:|:
Db        120 APNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQ 179

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                 | |||| |||| | : ||||::|||:||||:|| ||| ||:|||| |
Db        180 THREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIK 229


RESULT 12
GC1_MOUSE
ID   GC1_MOUSE      STANDARD;      PRT;   324 AA.
AC   P01868;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ig gamma-1 chain C region secreted form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=80045036; PubMed=115593;
RA   Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA   Takahashi N., Mano Y.;
RT   "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT   gamma 1 chain gene.";
RL   Cell 18:559-568(1979).
RN   [2]
RP   SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX   MEDLINE=80202559; PubMed=6769752;
RA   Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA   Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT   "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
RT   cloned in a bacterial plasmid.";
RL   Gene 9:87-97(1980).
RN   [3]
RP   SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX   MEDLINE=80012837; PubMed=113776;
RA   Rogers J., Clarke P., Salser W.;
RT   "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
RT   heavy chain.";
RL   Nucleic Acids Res. 6:3305-3321(1979).
RN   [4]
RP   SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX   MEDLINE=78242288; PubMed=98524;
RA   Adetugbo K.;
RT   "Evolution of immunoglobulin subclasses. Primary structure of a
RT   murine myeloma gammal chain.";
RL   J. Biol. Chem. 253:6068-6075(1978).
RN   [5]
RP   DISULFIDE BONDS (MOPC 21).
RX   MEDLINE=73008889; PubMed=5073237;
RA   Svasti J., Milstein C.;
RT   "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL   Biochem. J. 126:837-850(1972).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Secreted;
CC         IsoId=P01868-1; Sequence=Displayed;
CC         Note=May be the major isoform;
CC       Name=Membrane-bound;
CC         IsoId=P01869-1; Sequence=External;
CC   ------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; V00793; CAA24172.1; -.
DR   EMBL; V00793; CAA24173.1; -.
DR   EMBL; V00793; CAA24174.1; -.
DR   EMBL; V00793; CAA24175.1; -.
DR   EMBL; V00795; CAA24176.1; -.
DR   PIR; A02159; G1MS.
DR   GlycoSuiteDB; P01868; -.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Alternative splicing.
FT   NON_TER       1      1
FT   DOMAIN        1     97       CH1.
FT   DOMAIN       98    110       HINGE.
FT   DOMAIN      111    217       CH2.
FT   DOMAIN      218    324       CH3.
FT   DISULFID     27     82
FT   DISULFID    102    102       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID    104    104       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    107    107       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    138    198
FT   CARBOHYD    174    174       N-LINKED (GLCNAC. . .).
FT                                /FTId=CAR_000055.
FT   DISULFID    244    302
FT   MOD_RES     324    324       REMOVED POST-TRANSLATIONALLY.
FT   CONFLICT    276    276       N -> D (IN REF. 3).
FT   CONFLICT    278    278       N -> D (IN REF. 3).
SQ   SEQUENCE   324 AA;  35704 MW;  A338812F3D1F2C93 CRC64;

  Query Match             67.5%;  Score 396;  DB 1;  Length 324;
```

```
  Best Local Similarity   67.6%;  Pred. No. 9.7e-33;
  Matches   69;  Conservative   19;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          9 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 68
              |||:|||||||  | |:  ||:||||||||:|  :||||:|:|:||  ||||  |:|:|||||:||
Db        116 SVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNS 175

Qy         69 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |:|  ||  |  ::|||||||||:||:|::    |: ||||||  |
Db        176 TFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTK 217


RESULT 13
GCC_RAT
ID   GCC_RAT        STANDARD;      PRT;   329 AA.
AC   P20762;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig gamma-2C chain C region.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88166903; PubMed=3127222;
RA   Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
RT   "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
RT   region cDNA: extensive homology to mouse gamma 3.";
RL   Eur. J. Immunol. 18:317-319(1988).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X07189; CAA30169.1; -.
DR   PIR; S00847; S00847.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region.
FT   NON_TER       1      1
FT   DOMAIN        1     97       CH1.
FT   DOMAIN       98    113       HINGE.
FT   DOMAIN      114    222       CH2.
FT   DOMAIN      223    329       CH3.
FT   DISULFID     15     15       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     82
FT   DISULFID    111    111       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    113    113       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    143    203
FT   DISULFID    249    307
SQ   SEQUENCE   329 AA;  36571 MW;  5FCD7B7933850773 CRC64;

  Query Match             67.5%;  Score 396;  DB 1;  Length 329;
  Best Local Similarity   67.6%;  Pred. No. 9.9e-33;
  Matches   71;  Conservative   17;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          6 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 65
              | ||||:|||||| |||: ||:|||||||| |:|:|:|:|:|| | |  |:|:| |||
Db        118 GRPSVFIFPPKPKDILMITLTPKVTCVVVDVSEEEPDVQFSWFVDNVRVFTAQTQPHEEQ 177

Qy         66 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
```

```
              | |:|||| | : ||||::|||:||||:|| ||| |||||||  :
Db        178 LNGTFRVVSTLHIQHQDWMSGKEFKCKVNNKDLPSPIEKTISKPR 222


RESULT 14
GC1M_MOUSE
ID   GC1M_MOUSE     STANDARD;      PRT;   393 AA.
AC   P01869;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig gamma-1 chain C region, membrane-bound form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=80045036; PubMed=115593;
RA   Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA   Takahashi N., Mano Y.;
RT   "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT   gamma 1 chain gene.";
RL   Cell 18:559-568(1979).
RN   [2]
RP   SEQUENCE OF 323-393 FROM N.A.
RX   MEDLINE=82197626; PubMed=6804950;
RA   Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RT   "mRNA for surface immunoglobulin gamma chains encodes a highly
RT   conserved transmembrane sequence and a 28-residue intracellular
RT   domain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
RN   [3]
RP   SEQUENCE OF 323-366 FROM N.A.
RX   MEDLINE=82115295; PubMed=6799207;
RA   Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA   Eisenberg D., Wall R.;
RT   "Gene segments encoding transmembrane carboxyl termini of
RT   immunoglobulin gamma chains.";
RL   Cell 26:19-27(1981).
RN   [4]
RP   SEQUENCE OF 1-44 FROM N.A.
RX   MEDLINE=82222190; PubMed=6283537;
RA   Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT   "Nucleotide sequences of gene segments encoding membrane domains of
RT   immunoglobulin gamma chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Membrane-bound;
CC         IsoId=P01869-1; Sequence=Displayed;
CC       Name=Secreted;
CC         IsoId=P01868-1; Sequence=External;
CC         Note=May be the major isoform;
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; V00793; CAA24172.1; -.
DR   EMBL; V00793; CAA24173.1; -.
DR   EMBL; V00793; CAA24174.1; -.
DR   PIR; B02159; G1MSM.
DR   PDB; 1SC8; 23-MAR-99.
DR   PDB; 1AE6; 18-MAR-98.
DR   PDB; 1CL7; 12-JAN-00.
DR   PDB; 1F11; 06-FEB-01.
DR   PDB; 1F58; 29-DEC-99.
DR   PDB; 1KC5; 24-JUL-02.
```

```
DR   PDB; 1KCR; 11-MAY-02.
DR   PDB; 25C8; 09-JUL-99.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Alternative splicing; Transmembrane; 3D-structure.
FT   NON_TER       1      1
FT   DOMAIN        1     97       CH1.
FT   DOMAIN       98    110       HINGE.
FT   DOMAIN      111    217       CH2.
FT   DOMAIN      218    324       CH3.
FT   DISULFID     27     82
FT   DISULFID    102    102       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID    104    104       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    107    107       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    138    198
FT   CARBOHYD    174    174       N-LINKED (GLCNAC. . .).
FT   DISULFID    244    302
FT   TRANSMEM    340    357       POTENTIAL.
FT   DOMAIN      358    393       CYTOPLASMIC (POTENTIAL).
SQ   SEQUENCE   393 AA;  43386 MW;  4CC88343B7A1CE27 CRC64;

  Query Match             67.5%;  Score 396;  DB 1;  Length 393;
  Best Local Similarity   67.6%;  Pred. No. 1.2e-32;
  Matches   69;  Conservative   19;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          9 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 68
              |||:|||||||  | |: ||:||||||||:| :||||:|:|:|:|| |||| |:|:|||||:||
Db        116 SVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNS 175

Qy         69 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |:| || | ::||||||||||:||:|::   |: |||||||  |
Db        176 TFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTK 217


RESULT 15
GCAB_MOUSE
ID   GCAB_MOUSE     STANDARD;      PRT;   335 AA.
AC   P01864;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ig gamma-2A chain C region secreted form (B allele).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=82037861; PubMed=6170065;
RA   Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT   "Multiple differences between the nucleic acid sequences of the
RT   IgG2aa and IgG2ab alleles of the mouse.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN   [2]
RP   SEQUENCE.
RX   MEDLINE=82037777; PubMed=6794027;
RA   Dognin M.J., Lauwereys M., Strosberg A.D.;
RT   "Multiple amino acid substitutions between murine gamma 2a heavy
RT   chain Fc regions of Ig1a and Ig1b allotypic forms.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Secreted;
CC         IsoId=P01864-1; Sequence=Displayed;
CC         Note=Probably the major isoform;
CC       Name=Membrane-bound;
CC         IsoId=P01865-1; Sequence=External;
CC   -!- MISCELLANEOUS: The sequence differs from that of the a allele,
CC       from BALB/c mice, at 15% of the positions.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00479; -; NOT_ANNOTATED_CDS.
DR   PIR; A02153; G2MSAB.
DR   PDB; 1BOG; 23-MAR-99.
DR   PDB; 1HH6; 26-JAN-01.
DR   PDB; 1HH9; 24-JUL-03.
DR   PDB; 1HI6; 08-FEB-01.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Alternative splicing;
KW   3D-structure; Repeat.
FT   NON_TER       1      1
FT   DOMAIN        6     98       IG-LIKE 1.
FT   DOMAIN      126    225       IG-LIKE 2.
FT   DOMAIN      234    330       IG-LIKE 3.
SQ   SEQUENCE   335 AA;  36596 MW;  FA3382792CBB13C6 CRC64;

  Query Match             67.1%;  Score 394;  DB 1;  Length 335;
  Best Local Similarity   64.5%;  Pred. No. 1.6e-32;
  Matches   71;  Conservative   18;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||:|||| || |||| :| |||||||||| :||:|: :|:|: |||| |:|:
Db        119 APDLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQ 178

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                | |||| |||| | : ||||::|||:||||:|: ||| |||||||  :
Db        179 THREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNRALPSPIEKTISKPR 228


Search completed: April 29, 2004, 08:44:53
Job time : 10 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 29, 2004, 08:41:02 ; Search time 36 Seconds
(without alignments)
964.083 Million cell updates/sec

Title: US-09-674-857-3
Perfect score: 587
Sequence: 1 APPVAGGPSVFLFPPKPKDT.....CKVSNKGLPSSIEKTISKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	557	94.9	469	4	Q7Z7P5	Q7z7p5 homo sapien
2	557	94.9	470	4	Q7Z5W1	Q7z5w1 homo sapien
3	557	94.9	482	4	Q7Z351	Q7z351 homo sapien
4	557	94.9	679	4	Q96PQ8	Q96pq8 homo sapien
5	553	94.2	473	4	Q8TC63	Q8tc63 homo sapien
6	539	91.8	354	4	Q86TT2	Q86tt2 homo sapien
7	535	91.1	509	4	Q8NF17	Q8nf17 homo sapien
8	535	91.1	521	4	Q8N4Y9	Q8n4y9 homo sapien
9	458	78.0	337	6	Q95M34	Q95m34 equus cabal
10	418	71.2	470	11	Q7TMK1	Q7tmk1 mus musculu
11	400	68.1	469	11	Q8R3V9	Q8r3v9 mus musculu
12	397	67.6	473	11	Q91Z05	Q91z05 mus musculu
13	397	67.6	474	11	Q8R3H6	Q8r3h6 mus musculu
14	396	67.5	437	11	Q9R1A4	Q9r1a4 mus musculu
15	396	67.5	463	11	Q99LC4	Q99lc4 mus musculu
16	394	67.1	473	11	Q9D8L4	Q9d8l4 mus musculu
17	382	65.1	468	11	Q99L31	Q99l31 mus musculu
18	382	65.1	473	11	Q99L25	Q99l25 mus musculu
19	138	23.5	375	4	Q86TT1	Q86tt1 homo sapien
20	138	23.5	588	4	Q8WUX4	Q8wux4 homo sapien
21	138	23.5	597	4	Q9BU10	Q9bu10 homo sapien
22	138	23.5	597	4	Q9BQB8	Q9bqb8 homo sapien
23	138	23.5	597	4	Q96BB9	Q96bb9 homo sapien
24	138	23.5	613	4	Q96EY0	Q96ey0 homo sapien
25	138	23.5	613	4	Q8WUK1	Q8wuk1 homo sapien
26	138	23.5	614	4	Q96GA6	Q96ga6 homo sapien
27	138	23.5	618	4	Q96AA6	Q96aa6 homo sapien
28	132	22.5	613	11	Q8VCX7	Q8vcx7 mus musculu
29	132	22.5	614	11	Q7TMT6	Q7tmt6 mus musculu
30	131	22.3	234	4	Q7Z473	Q7z473 homo sapien
31	131	22.3	236	4	Q7Z3Y4	Q7z3y4 homo sapien
32	131	22.3	239	4	Q8NEK0	Q8nek0 homo sapien
33	131	22.3	239	4	Q8TCD0	Q8tcd0 homo sapien
34	123.5	21.0	478	4	Q7Z379	Q7z379 homo sapien
35	122.5	20.9	684	13	Q90544	Q90544 ginglymosto
36	121.5	20.7	130	11	Q9D8W4	Q9d8w4 mus musculu
37	120	20.4	497	4	Q8WY24	Q8wy24 homo sapien
38	119.5	20.4	384	4	Q9UP60	Q9up60 homo sapien
39	119.5	20.4	416	4	Q9NPP6	Q9npp6 homo sapien
40	119.5	20.4	492	4	Q7Z374	Q7z374 homo sapien
41	119.5	20.4	493	4	Q8NCL6	Q8ncl6 homo sapien
42	119.5	20.4	494	4	Q96K68	Q96k68 homo sapien
43	119.5	20.4	496	4	Q96DK0	Q96dk0 homo sapien
44	119.5	20.4	496	4	Q96KX8	Q96kx8 homo sapien
45	119.5	20.4	499	4	Q8N5K4	Q8n5k4 homo sapien

ALIGNMENTS

RESULT 1
Q7Z7P5
ID Q7Z7P5 PRELIMINARY; PRT; 469 AA.
AC Q7Z7P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;

```
RA   Strausberg R.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC051328; AAH51328.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   469 AA;  51395 MW;  C8D5BE12BAAF795C CRC64;

  Query Match             94.9%;  Score 557;  DB 4;  Length 469;
  Best Local Similarity   94.5%;  Pred. No. 9e-54;
  Matches  104;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 312

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||| ||: |||||||||
Db        313 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 362


RESULT 2
Q7Z5W1
ID   Q7Z5W1      PRELIMINARY;      PRT;   470 AA.
AC   Q7Z5W1;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC053984; AAH53984.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51204 MW;  778CF34521483E1A CRC64;

  Query Match             94.9%;  Score 557;  DB 4;  Length 470;
  Best Local Similarity   94.5%;  Pred. No. 9e-54;
  Matches  104;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 313

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||| ||: |||||||||
Db        314 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 363


RESULT 3
Q7Z351
ID   Q7Z351      PRELIMINARY;      PRT;   482 AA.
AC   Q7Z351;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein DKFZp686N02209.
GN   DKFZP686N02209.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human rectum tumor;
RA   Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX538118; CAD98026.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   482 AA;  52852 MW;  EDA75F1901D1A034 CRC64;

  Query Match             94.9%;  Score 557;  DB 4;  Length 482;
  Best Local Similarity   94.5%;  Pred. No. 9.3e-54;
  Matches  104;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 325

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||| ||: |||||||||
Db        326 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 375


RESULT 4
Q96PQ8
ID   Q96PQ8      PRELIMINARY;      PRT;   679 AA.
AC   Q96PQ8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Factor VII active site mutant immunoconjugate.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21477448; PubMed=11593034;
RA   Hu Z., Garen A.;
RT   "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT   cells for immunotherapy in mouse models of prostatic cancer.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Hu Z., Garen A.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF272774; AAK58686.2; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR000152; Asx_hydroxyl_S.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR001881; EGF_Ca.
```

```
DR   InterPro; IPR001438; EGF_II.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002383; GLA_blood.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR000294; VitK_dep_GLA.
DR   Pfam; PF00008; EGF; 2.
DR   Pfam; PF00594; gla; 1.
DR   Pfam; PF00047; ig; 2.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00010; EGFBLOOD.
DR   PRINTS; PR00001; GLABLOOD.
DR   SMART; SM00181; EGF; 2.
DR   SMART; SM00179; EGF_CA; 1.
DR   SMART; SM00069; GLA; 1.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00010; ASX_HYDROXYL; 1.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01187; EGF_CA; 1.
DR   PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
SQ   SEQUENCE   679 AA;  75552 MW;  0B0023AE70A067A1 CRC64;

  Query Match             94.9%;  Score 557;  DB 4;  Length 679;
  Best Local Similarity   94.5%;  Pred. No. 1.4e-53;
  Matches  104;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 522

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||| ||: |||||||||
Db        523 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 572


RESULT 5
Q8TC63
ID   Q8TC63      PRELIMINARY;      PRT;   473 AA.
AC   Q8TC63;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC025985; AAH25985.1; -.
DR   GO; GO:0005507; F:copper ion binding; IEA.
DR   GO; GO:0005489; F:electron transporter activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR000923; BlueCu_1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00196; COPPER_BLUE; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;  51986 MW;  E29920B09BA369F5 CRC64;

  Query Match             94.2%;  Score 553;  DB 4;  Length 473;
  Best Local Similarity   94.5%;  Pred. No. 2.6e-53;
  Matches  104;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              ||   |||||||||||||||||||||||||||||||||| |||||:|||||||||||||||
Db        257 APEPLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 316

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||:|||||||||||||||||||||||||||||||||||||||||||||
Db        317 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 366


RESULT 6
Q86TT2
ID   Q86TT2      PRELIMINARY;      PRT;   354 AA.
AC   Q86TT2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Human full-length cDNA clone CS0DI019YF20 of placenta of Homo sapiens
DE   (Human) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RA   Genoscope;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RA   Li W.B., Gruber C., Jessee J., Polayes D.;
RT   "Full-length cDNA libraries and normalization.";
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX248278; CAD62606.1; -.
DR   GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00407; IGc1; 3.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Plasmid.
FT   NON_TER      1      1
SQ   SEQUENCE   354 AA;  39125 MW;  23B80BF4D2B87A92 CRC64;

  Query Match             91.8%;  Score 539;  DB 4;  Length 354;
  Best Local Similarity   90.9%;  Pred. No. 6.6e-52;
  Matches  100;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||:| ||||||||||||||
Db        138 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 197

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||:|||||||||||||||||||||||| ||: ||||||| |
Db        198 PREEQYNSTPRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 247


RESULT 7
Q8NF17
ID   Q8NF17      PRELIMINARY;      PRT;   509 AA.
```

```
AC   Q8NF17;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   FLJ00385 protein (Fragment).
GN   FLJ00385.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RT   "The nucleotide sequence of a long cDNA clone isolated from human
RT   spleen.";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK090464; BAC03445.1; -.
DR   PIR; A45874; A45874.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 3.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
FT   NON_TER       1      1
SQ   SEQUENCE   509 AA;  56111 MW;  089498D8076E863C CRC64;

  Query Match             91.1%;  Score 535;  DB 4;  Length 509;
  Best Local Similarity   90.0%;  Pred. No. 2.9e-51;
  Matches   99;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||:| ||||||||||||||
Db        224 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 283

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||:|||:|||||||||||||||||||||||| ||: ||||||| |
Db        284 PREEQFNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 333


RESULT 8
Q8N4Y9
ID   Q8N4Y9       PRELIMINARY;      PRT;   521 AA.
AC   Q8N4Y9;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC033178; AAH33178.1; -.
DR   PIR; A60764; A60764.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   521 AA;  57156 MW;  2AC7D22E72D6CAA2 CRC64;

  Query Match             91.1%;  Score 535;  DB 4;  Length 521;
  Best Local Similarity   90.0%;  Pred. No. 3e-51;
  Matches   99;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||:| ||||||||||||||
Db        305 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 364

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||:|||:|||||||||||||||||||||||| ||: ||||||| |
Db        365 PREEQFNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 414


RESULT 9
Q95M34
ID   Q95M34       PRELIMINARY;      PRT;   337 AA.
AC   Q95M34;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Immunogobulin gamma 1 heavy chain constant region (Fragment).
GN   IGHC1.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wagner B.;
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98383416; PubMed=9717671;
RA   Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA   Leibold W., Radbruch A.;
RT   "Organization of the equine immunoglobulin heavy chain constant region
RT   genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL   Immunobiology 199:105-119(1998).
DR   EMBL; AJ300675; CAC44624.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
FT   NON_TER       1      1
SQ   SEQUENCE   337 AA;  37438 MW;  A60BF2B01DEFD1F6 CRC64;

  Query Match             78.0%;  Score 458;  DB 6;  Length 337;
  Best Local Similarity   73.6%;  Pred. No. 7.4e-43;
  Matches   81;  Conservative   16;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : ||||||:||| |||||||:|||||||||||||| |:|:||||||:||||| | |:
Db        119 APELLGGPSVFIFPPNPKDTLMITRTPEVTCVVVDVSQENPDVKFNWYMDGVEVRTATTR 178

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |:|||:|||||||||| : |||||:|||:||||:|: ||  ||:||:| |
Db        179 PKEEQFNSTYRVVSVLRIQHQDWLSGKEFKCKVNNQALPQPIERTITKTK 228


RESULT 10
Q7TMK1
ID   Q7TMK1       PRELIMINARY;      PRT;   470 AA.
AC   Q7TMK1;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Breast tumor;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Breast tumor;
RA   Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC055910; AAH55910.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51727 MW;  6D90E4DF896BB090 CRC64;

  Query Match             71.2%;  Score 418;  DB 11;  Length 470;
  Best Local Similarity   68.5%;  Pred. No. 3.4e-38;
  Matches   76;  Conservative   15;  Mismatches   18;  Indels    2;  Gaps    1;

Qy          2 PP--VAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 59
              ||  : |||||||:|||||||  |||| ||:|||||||| :||:|  :|:||  ||| | |
Db        253 PPGNILGGPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWT 312

Qy         60 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              :||| |||||:|||| | : ||||: |||:||||:|| ||: ||:|||| |
Db        313 QPREAQYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPK 363


RESULT 11
Q8R3V9
ID   Q8R3V9      PRELIMINARY;      PRT;   469 AA.
AC   Q8R3V9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   IGH-4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC024405; AAH24405.1; -.
DR   PIR; B45837; B45837.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   469 AA;  51976 MW;  534793F155D05457 CRC64;

  Query Match             68.1%;  Score 400;  DB 11;  Length 469;
  Best Local Similarity   68.6%;  Pred. No. 3.5e-36;
  Matches   70;  Conservative   18;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          9 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 68
              |||:|||||| | |: ||:||||||:| :||||:|:|:|| |||| |:|||||||:||
Db        261 SVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTKPREEQFNS 320

Qy         69 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |:| || | ::|||||||||:||:|::   |: |||||| |
Db        321 TFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTK 362


RESULT 12
Q91Z05
ID   Q91Z05      PRELIMINARY;      PRT;   473 AA.
AC   Q91Z05;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   AU044919.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC010327; AAH10327.1; -.
DR   MGD; MGI:2144967; AU044919.
DR   GO; GO:0005489; F:electron transporter activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR000345; CytC_heme_BS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00190; CYTOCHROME_C; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;  51946 MW;  CF625F008932AF12 CRC64;

  Query Match             67.6%;  Score 397;  DB 11;  Length 473;
  Best Local Similarity   65.5%;  Pred. No. 7.6e-36;
  Matches   72;  Conservative   17;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : ||||||:|||  || |||| ||:|||||||||| :||:|: :|:|: |||| |:|:
Db        257 APNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQ 316

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                 | |||| |||| | : |||::|||:||||:|| ||| ||:|||| |
Db        317 THREDYNSTIRVVSALPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIK 366


RESULT 13
Q8R3H6
ID   Q8R3H6      PRELIMINARY;      PRT;   474 AA.
AC   Q8R3H6;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   AU044919.
OS   Mus musculus (Mouse).
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC025447; AAH25447.1; -.
DR   MGD; MGI:2144967; AU044919.
DR   GO; GO:0005489; F:electron transporter activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR000345; CytC_heme_BS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00190; CYTOCHROME_C; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   474 AA;  51748 MW;  8608B57C6CD2874A CRC64;

  Query Match             67.6%;  Score 397;  DB 11;  Length 474;
  Best Local Similarity   65.5%;  Pred. No. 7.6e-36;
  Matches   72;  Conservative   17;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||:|||  || |||| ||:||||||||| :||:|: :|:|: |||| |:|:
Db        258 APNLEGGPSVFIPPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQ 317

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                 | |||| |||| | : ||||::|||:||||:|| ||| ||:|||| |
Db        318 THREDYNSTIRVVSALPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIK 367


RESULT 14
Q9R1A4
ID   Q9R1A4      PRELIMINARY;      PRT;   437 AA.
AC   Q9R1A4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Gamma1 heavy chain of Mab7 (Fragment).
GN   IGH-4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT   "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT   antibody (Mab 7, its light and heavy chains) and construction of a
RT   single chain antibody (scFV).";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF152372; AAD40243.1; -.
DR   PIR; B45837; B45837.
DR   PDB; 1CQK; 11-SEP-99.
DR   PDB; 1I9I; 25-DEC-02.
DR   PDB; 1KCU; 11-MAY-02.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
FT   NON_TER       1       1
FT   NON_TER     437     437
SQ   SEQUENCE   437 AA;  48142 MW;  5C3A7BB3EE7D697C CRC64;

  Query Match             67.5%;  Score 396;  DB 11;  Length 437;
  Best Local Similarity   67.6%;  Pred. No. 8.9e-36;
  Matches   69;  Conservative   19;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          9 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 68
              |||:|||||| | |: ||:|||||||:| :||||:|:|:|| |||| |:|:|||||:||
Db        229 SVFIPPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNS 288

Qy         69 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |:| || | ::||||||||:||:|::   |: |||||| |
Db        289 TFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTK 330


RESULT 15
Q99LC4
ID   Q99LC4      PRELIMINARY;      PRT;   463 AA.
AC   Q99LC4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to RIKEN cDNA 1810060O09 gene.
GN   IGH-4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003435; AAH03435.1; -.
DR   PIR; B45837; B45837.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
SQ   SEQUENCE   463 AA;  51007 MW;  EAA674C6BBC30783 CRC64;

  Query Match             67.5%;  Score 396;  DB 11;  Length 463;
  Best Local Similarity   67.6%;  Pred. No. 9.6e-36;
  Matches   69;  Conservative   19;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          9 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 68
              |||:|||||| | |: ||:|||||||:| :||||:|:|:|| |||| |:|:|||||:||
Db        255 SVFIPPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNS 314

Qy         69 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |:| || | ::||||||||:||:|::   |: |||||| |
Db        315 TFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTK 356


Search completed: April 29, 2004, 08:46:18
Job time : 37 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 29, 2004, 08:46:23 ; Search time 38.5 Seconds
(without alignments)
791.970 Million cell updates/sec

Title: US-09-674-857-3
Perfect score: 587
Sequence: 1 APPVAGGPSVFLFPPKPKDT.....CKVSNKGLPSSIEKTISKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 277189581 residues

Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	570	97.1	435	10	US-09-932-812-22	Sequence 22, Appl
2	570	97.1	447	10	US-09-968-362-22	Sequence 22, Appl
3	562	95.7	468	14	US-10-071-485-67	Sequence 67, Appl
4	562	95.7	488	12	US-10-683-255-12	Sequence 12, Appl
5	562	95.7	497	12	US-10-683-255-10	Sequence 10, Appl
6	562	95.7	525	12	US-10-683-255-8	Sequence 8, Appli
7	562	95.7	711	14	US-10-071-485-90	Sequence 90, Appl
8	558	95.1	232	14	US-10-008-063-28	Sequence 28, Appl
9	558	95.1	232	14	US-10-008-063-32	Sequence 32, Appl
10	558	95.1	250	14	US-10-152-363A-35	Sequence 35, Appl
11	558	95.1	251	14	US-10-152-363A-31	Sequence 31, Appl
12	558	95.1	251	14	US-10-152-363A-33	Sequence 33, Appl
13	558	95.1	328	14	US-10-008-063-42	Sequence 42, Appl
14	558	95.1	332	14	US-10-152-363A-62	Sequence 62, Appl
15	558	95.1	344	14	US-10-152-363A-52	Sequence 52, Appl
16	558	95.1	348	14	US-10-152-363A-54	Sequence 54, Appl
17	558	95.1	357	14	US-10-152-363A-56	Sequence 56, Appl
18	558	95.1	392	14	US-10-152-363A-50	Sequence 50, Appl
19	558	95.1	437	10	US-09-932-812-20	Sequence 20, Appl
20	558	95.1	449	10	US-09-968-362-20	Sequence 20, Appl
21	558	95.1	473	10	US-09-995-898A-23	Sequence 23, Appl
22	558	95.1	473	12	US-10-420-034A-23	Sequence 23, Appl
23	558	95.1	476	10	US-09-925-055D-23	Sequence 23, Appl
24	558	95.1	476	14	US-10-104-919-62	Sequence 62, Appl
25	558	95.1	476	16	US-10-395-741B-63	Sequence 63, Appl
26	558	95.1	484	10	US-09-925-055D-30	Sequence 30, Appl
27	558	95.1	484	14	US-10-104-919-61	Sequence 61, Appl
28	558	95.1	484	16	US-10-395-741B-62	Sequence 62, Appl
29	558	95.1	559	9	US-09-746-359A-62	Sequence 62, Appl
30	558	95.1	559	12	US-09-951-268-39	Sequence 39, Appl
31	558	95.1	559	15	US-10-424-658-62	Sequence 62, Appl
32	558	95.1	594	9	US-09-746-359A-23	Sequence 23, Appl
33	558	95.1	594	12	US-09-951-268-24	Sequence 24, Appl
34	558	95.1	594	15	US-10-424-658-23	Sequence 23, Appl
35	558	95.1	764	10	US-09-892-949-69	Sequence 69, Appl
36	558	95.1	764	12	US-10-352-554-39	Sequence 39, Appl
37	558	95.1	764	15	US-10-351-157-39	Sequence 39, Appl
38	557	94.9	110	15	US-10-370-749-23	Sequence 23, Appl
39	557	94.9	212	13	US-10-033-522-2	Sequence 2, Appli
40	557	94.9	215	15	US-10-264-049-4290	Sequence 4290, Ap
41	557	94.9	218	12	US-09-813-341-1	Sequence 1, Appli
42	557	94.9	218	12	US-09-813-341-2	Sequence 2, Appli
43	557	94.9	218	14	US-10-277-307-1	Sequence 1, Appli
44	557	94.9	218	14	US-10-277-307-2	Sequence 2, Appli
45	557	94.9	218	14	US-10-277-370-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-932-812-22
; Sequence 22, Application US/09932812
; Publication No. US20030082749A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biolog
; FILE REFERENCE: 02SUN2001
; CURRENT APPLICATION NUMBER: US/09/932,812
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HuEPO-L-vFc gamma1 with a 27-amino acid leader peptide (Figure 2
US-09-932-812-22

Query Match 97.1%; Score 570; DB 10; Length 435;
Best Local Similarity 97.3%; Pred. No. 1.6e-50;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 APEVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 278

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||||| ||:|||||||||
Db        279 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK 328
```

RESULT 2
US-09-968-362-22
; Sequence 22, Application US/09968362

; Publication No. US20030082679A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulaing factor
; TITLE OF INVENTION: biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/09/968,362
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hG-CSF-L-vFc gamma1 with a 30-amino acid leader peptide (Figure 2
; OTHER INFORMATION: C)
US-09-968-362-22

Query Match 97.1%; Score 570; DB 10; Length 447;
Best Local Similarity 97.3%; Pred. No. 1.6e-50;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 231 APEVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 290

Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
Db 291 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK 340

RESULT 3
US-10-071-485-67
; Sequence 67, Application US/10071485
; Publication No. US20030099648A1
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-67

Query Match 95.7%; Score 562; DB 14; Length 468;
Best Local Similarity 95.5%; Pred. No. 1.1e-49;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 251 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 310

Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
Db 311 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK 360

RESULT 4
US-10-683-255-12
; Sequence 12, Application US/10683255
; Publication No. US20040063910A1
; GENERAL INFORMATION:
; APPLICANT: Kavanaugh, William M.
; APPLICANT: Ballinger, Marcus
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
; TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
; FILE REFERENCE: PP01474.101
; CURRENT APPLICATION NUMBER: US/10/683,255
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 09/499,846
; PRIOR FILING DATE: 2000-02-07
; PRIOR APPLICATION NUMBER: 60/119,002
; PRIOR FILING DATE: 1999-02-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-683-255-12

Query Match 95.7%; Score 562; DB 12; Length 488;
Best Local Similarity 95.5%; Pred. No. 1.2e-49;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 272 APELEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 331

Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
Db 332 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK 381

RESULT 5
US-10-683-255-10
; Sequence 10, Application US/10683255
; Publication No. US20040063910A1
; GENERAL INFORMATION:
; APPLICANT: Kavanaugh, William M.
; APPLICANT: Ballinger, Marcus
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
; TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
; FILE REFERENCE: PP01474.101
; CURRENT APPLICATION NUMBER: US/10/683,255
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 09/499,846
; PRIOR FILING DATE: 2000-02-07
; PRIOR APPLICATION NUMBER: 60/119,002
; PRIOR FILING DATE: 1999-02-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-683-255-10

Query Match 95.7%; Score 562; DB 12; Length 497;
Best Local Similarity 95.5%; Pred. No. 1.2e-49;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 281 APELEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 340

```
Qy          61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
               ||||||||||||||||||||||||||||||||||||||||||||| ||:||||||||||
Db         341 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK 390
```

RESULT 6
US-10-683-255-8
; Sequence 8, Application US/10683255
; Publication No. US20040063910A1
; GENERAL INFORMATION:
; APPLICANT: Kavanaugh, William M.
; APPLICANT: Ballinger, Marcus
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
; TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
; FILE REFERENCE: PP01474.101
; CURRENT APPLICATION NUMBER: US/10/683,255
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 09/499,846
; PRIOR FILING DATE: 2000-02-07
; PRIOR APPLICATION NUMBER: 60/119,002
; PRIOR FILING DATE: 1999-02-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-683-255-8

Query Match 95.7%; Score 562; DB 12; Length 525;
Best Local Similarity 95.5%; Pred. No. 1.3e-49;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy           1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
               || : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         309 APELEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 368

Qy          61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
               ||||||||||||||||||||||||||||||||||||||||||||| ||:||||||||||
Db         369 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK 418
```

RESULT 7
US-10-071-485-90
; Sequence 90, Application US/10071485
; Publication No. US20030099648A1
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-90

Query Match 95.7%; Score 562; DB 14; Length 711;
Best Local Similarity 95.5%; Pred. No. 1.9e-49;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy           1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
               || : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         251 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 310

Qy          61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
               ||||||||||||||||||||||||||||||||||||||||||||| ||:||||||||||
Db         311 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK 360
```

RESULT 8
US-10-008-063-28
; Sequence 28, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Henne, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified immunoglobulin moiety.
US-10-008-063-28

Query Match 95.1%; Score 558; DB 14; Length 232;
Best Local Similarity 95.5%; Pred. No. 1.3e-49;
Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy           1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
               ||   | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          16 APEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 75

Qy          61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
               |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db          76 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAK 125
```

RESULT 9
US-10-008-063-32
; Sequence 32, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Henne, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified immunoglobulin moiety.
US-10-008-063-32

```
  Query Match             95.1%;  Score 558;  DB 14;  Length 232;
  Best Local Similarity   95.5%;  Pred. No. 1.3e-49;
  Matches  105;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              ||   | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 APEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 75

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||| ||||||||||||
Db         76 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAK 125


RESULT 10
US-10-152-363A-35
; Sequence 35, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
;  APPLICANT: Rixon, Mark W.
;  APPLICANT:  Gross, Jane A.
;  TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
;  FILE REFERENCE: 01-20
;  CURRENT APPLICATION NUMBER: US/10/152,363A
;  CURRENT FILING DATE:  2002-05-20
;  PRIOR APPLICATION NUMBER: 60/293,343
;  PRIOR FILING DATE: 2001-05-24
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 35
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Modified immunoglobulin moiety.
US-10-152-363A-35

  Query Match             95.1%;  Score 558;  DB 14;  Length 250;
  Best Local Similarity   95.5%;  Pred. No. 1.4e-49;
  Matches  105;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              ||   | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         35 APEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 94

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||| ||||||||||||
Db         95 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAK 144


RESULT 11
US-10-152-363A-31
; Sequence 31, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
;  APPLICANT: Rixon, Mark W.
;  APPLICANT:  Gross, Jane A.
;  TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
;  FILE REFERENCE: 01-20
;  CURRENT APPLICATION NUMBER: US/10/152,363A
;  CURRENT FILING DATE:  2002-05-20
;  PRIOR APPLICATION NUMBER: 60/293,343
;  PRIOR FILING DATE: 2001-05-24
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 31
;   LENGTH: 251
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Modified immunoglobulin moiety.
US-10-152-363A-31

  Query Match             95.1%;  Score 558;  DB 14;  Length 251;
  Best Local Similarity   95.5%;  Pred. No. 1.4e-49;
  Matches  105;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              ||   | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         35 APEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 94

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||| ||||||||||||
Db         95 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAK 144


RESULT 12
US-10-152-363A-33
; Sequence 33, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
;  APPLICANT: Rixon, Mark W.
;  APPLICANT:  Gross, Jane A.
;  TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
;  FILE REFERENCE: 01-20
;  CURRENT APPLICATION NUMBER: US/10/152,363A
;  CURRENT FILING DATE:  2002-05-20
;  PRIOR APPLICATION NUMBER: 60/293,343
;  PRIOR FILING DATE: 2001-05-24
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
;   LENGTH: 251
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Modified immunoglobulin moiety.
US-10-152-363A-33

  Query Match             95.1%;  Score 558;  DB 14;  Length 251;
  Best Local Similarity   95.5%;  Pred. No. 1.4e-49;
  Matches  105;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              ||   | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         35 APEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 94

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||| ||||||||||||
Db         95 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAK 144


RESULT 13
US-10-008-063-42
; Sequence 42, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
;  APPLICANT: Gross, Jane A.
;  APPLICANT:  Xu, Wenfeng
;  APPLICANT:  Henne, Randal M.
;  APPLICANT:  Grant, Francis, J.
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
;  FILE REFERENCE: 00-103
;  CURRENT APPLICATION NUMBER: US/10/008,063
;  CURRENT FILING DATE:  2001-11-05
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
;   LENGTH: 328
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Ztnfr12-tcs-Fc5.
US-10-008-063-42

  Query Match             95.1%;  Score 558;  DB 14;  Length 328;
  Best Local Similarity   95.5%;  Pred. No. 2e-49;
```

```
  Matches  105;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              ||   | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 APEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 171

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||| ||||||||||||
Db        172 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAK 221


RESULT 14
US-10-152-363A-62
; Sequence 62, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
;  APPLICANT: Rixon, Mark W.
;  APPLICANT:  Gross, Jane A.
;  TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
;  FILE REFERENCE: 01-20
;  CURRENT APPLICATION NUMBER: US/10/152,363A
;  CURRENT FILING DATE:  2002-05-20
;  PRIOR APPLICATION NUMBER: 60/293,343
;  PRIOR FILING DATE: 2001-05-24
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 62
;   LENGTH: 332
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fusion protein.
US-10-152-363A-62

  Query Match             95.1%;  Score 558;  DB 14;  Length 332;
  Best Local Similarity   95.5%;  Pred. No. 2e-49;
  Matches  105;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              ||   | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        116 APEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 175

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||| ||||||||||||
Db        176 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAK 225


RESULT 15
US-10-152-363A-52
; Sequence 52, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
;  APPLICANT: Rixon, Mark W.
;  APPLICANT:  Gross, Jane A.
;  TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
;  FILE REFERENCE: 01-20
;  CURRENT APPLICATION NUMBER: US/10/152,363A
;  CURRENT FILING DATE:  2002-05-20
;  PRIOR APPLICATION NUMBER: 60/293,343
;  PRIOR FILING DATE: 2001-05-24
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 52
;   LENGTH: 344
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fusion protein.
US-10-152-363A-52

  Query Match             95.1%;  Score 558;  DB 14;  Length 344;
  Best Local Similarity   95.5%;  Pred. No. 2.1e-49;
  Matches  105;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              ||   | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 APEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 187

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||| ||||||||||||
Db        188 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAK 237


Search completed: April 29, 2004, 08:55:54
Job time : 39.5 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 29, 2004, 08:42:33 ; Search time 16.5 Seconds
(without alignments)
344.173 Million cell updates/sec

Title: US-09-674-857-3
Perfect score: 587
Sequence: 1 APPVAGGPSVFLFPPKPKDT.....CKVSNKGLPSSIEKTISKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	562	95.7	468	4	US-09-485-737B-67	Sequence 67, Appl
2	562	95.7	488	4	US-09-499-846-12	Sequence 12, Appl
3	562	95.7	497	4	US-09-499-846-10	Sequence 10, Appl
4	562	95.7	525	4	US-09-499-846-8	Sequence 8, Appli
5	562	95.7	711	4	US-09-485-737B-90	Sequence 90, Appl
6	558	95.1	559	4	US-09-746-359A-62	Sequence 62, Appl
7	558	95.1	594	4	US-09-746-359A-23	Sequence 23, Appl
8	557	94.9	110	3	US-08-444-644-21	Sequence 21, Appl
9	557	94.9	110	4	US-08-232-246A-21	Sequence 21, Appl
10	557	94.9	116	2	US-08-232-539D-55	Sequence 55, Appl
11	557	94.9	212	1	US-08-430-633-4	Sequence 4, Appli
12	557	94.9	212	2	US-08-620-694A-4	Sequence 4, Appli
13	557	94.9	212	2	US-08-936-854-4	Sequence 4, Appli
14	557	94.9	212	3	US-09-022-255-4	Sequence 4, Appli
15	557	94.9	212	3	US-09-022-696-4	Sequence 4, Appli
16	557	94.9	212	3	US-09-022-253-4	Sequence 4, Appli
17	557	94.9	212	3	US-09-022-260-4	Sequence 4, Appli
18	557	94.9	212	3	US-09-022-259-4	Sequence 4, Appli
19	557	94.9	212	3	US-09-022-257-4	Sequence 4, Appli
20	557	94.9	212	4	US-09-549-679-4	Sequence 4, Appli
21	557	94.9	228	4	US-09-428-082B-2	Sequence 2, Appli
22	557	94.9	228	4	US-09-847-249A-2	Sequence 2, Appli
23	557	94.9	229	4	US-09-122-144-2	Sequence 2, Appli
24	557	94.9	232	2	US-08-595-043A-50	Sequence 50, Appl
25	557	94.9	235	3	US-09-131-247-6	Sequence 6, Appli
26	557	94.9	243	4	US-09-428-082B-1068	Sequence 1068, Ap
27	557	94.9	247	4	US-09-428-082B-6	Sequence 6, Appli
28	557	94.9	247	4	US-09-428-082B-12	Sequence 12, Appl
29	557	94.9	248	4	US-09-428-082B-1056	Sequence 1056, Ap
30	557	94.9	248	4	US-09-428-082B-1058	Sequence 1058, Ap
31	557	94.9	248	4	US-09-428-082B-1060	Sequence 1060, Ap
32	557	94.9	248	4	US-09-428-082B-1062	Sequence 1062, Ap
33	557	94.9	250	4	US-09-428-082B-1070	Sequence 1070, Ap
34	557	94.9	252	4	US-09-428-082B-1064	Sequence 1064, Ap
35	557	94.9	252	4	US-09-428-082B-1066	Sequence 1066, Ap
36	557	94.9	253	4	US-09-428-082B-16	Sequence 16, Appl
37	557	94.9	253	4	US-09-428-082B-18	Sequence 18, Appl
38	557	94.9	254	2	US-08-284-391B-33	Sequence 33, Appl
39	557	94.9	254	3	US-09-218-950-33	Sequence 33, Appl
40	557	94.9	268	4	US-09-428-082B-8	Sequence 8, Appli
41	557	94.9	269	4	US-09-428-082B-10	Sequence 10, Appl
42	557	94.9	277	4	US-09-428-082B-20	Sequence 20, Appl
43	557	94.9	277	4	US-09-428-082B-22	Sequence 22, Appl
44	557	94.9	316	3	US-09-178-869-4	Sequence 4, Appli
45	557	94.9	316	4	US-09-761-413-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-485-737B-67
; Sequence 67, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-67

Query Match 95.7%; Score 562; DB 4; Length 468;
Best Local Similarity 95.5%; Pred. No. 2.7e-58;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 310

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||| ||:|||||||||||
Db        311 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK 360
```

RESULT 2
US-09-499-846-12
; Sequence 12, Application US/09499846
; Patent No. 6656728
; GENERAL INFORMATION:
; APPLICANT: Kavanaugh et al.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
; TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
; FILE REFERENCE: 035784/195012 (5784-

; CURRENT APPLICATION NUMBER: US/09/499,846
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-499-846-12

Query Match 95.7%; Score 562; DB 4; Length 488;
Best Local Similarity 95.5%; Pred. No. 2.8e-58;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 APELEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 331

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||||| ||:||||||||||
Db        332 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK 381
```

RESULT 3
US-09-499-846-10
; Sequence 10, Application US/09499846
; Patent No. 6656728
; GENERAL INFORMATION:
; APPLICANT: Kavanaugh et al.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
; TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
; FILE REFERENCE: 035784/195012 (5784-
; CURRENT APPLICATION NUMBER: US/09/499,846
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-499-846-10

Query Match 95.7%; Score 562; DB 4; Length 497;
Best Local Similarity 95.5%; Pred. No. 2.9e-58;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 APELEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 340

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||||| ||:||||||||||
Db        341 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK 390
```

RESULT 4
US-09-499-846-8
; Sequence 8, Application US/09499846
; Patent No. 6656728
; GENERAL INFORMATION:
; APPLICANT: Kavanaugh et al.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
; TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
; FILE REFERENCE: 035784/195012 (5784-
; CURRENT APPLICATION NUMBER: US/09/499,846
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-499-846-8

Query Match 95.7%; Score 562; DB 4; Length 525;
Best Local Similarity 95.5%; Pred. No. 3.1e-58;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 APELEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 368

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||||| ||:||||||||||
Db        369 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK 418
```

RESULT 5
US-09-485-737B-90
; Sequence 90, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90

Query Match 95.7%; Score 562; DB 4; Length 711;
Best Local Similarity 95.5%; Pred. No. 4.7e-58;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 310

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||||| ||:||||||||||
Db        311 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK 360
```

RESULT 6
US-09-746-359A-62
; Sequence 62, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108

```
;  CURRENT APPLICATION NUMBER: US/09/746,359A
;  CURRENT FILING DATE:  2001-05-21
;  PRIOR APPLICATION NUMBER: 60/171,969
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/213,341
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 62
;   LENGTH: 559
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-746-359A-62

  Query Match             95.1%;  Score 558;  DB 4;  Length 559;
  Best Local Similarity   95.5%;  Pred. No. 1e-57;
  Matches  105;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              ||    | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 APEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 402

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        403 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAK 452


RESULT 7
US-09-746-359A-23
; Sequence 23, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
;  APPLICANT: Thompson, Penny
;  APPLICANT:  Foster, Donald C.
;  APPLICANT:  Xu, Wenfeng
;  APPLICANT:  Madden, Karen L.
;  APPLICANT:  Kelly, James D.
;  APPLICANT:  Sprecher, Cindy A.
;  APPLICANT:  Blumberg, Hal
;  APPLICANT:  Eagan, Maribeth A.
;  APPLICANT:  Jaspers, Stephen R.
;  APPLICANT:  Chandrasekher, Yasmin A.
;  APPLICANT:  No. 6610286ak, Julia E.
;  TITLE OF INVENTION: Method for Treating Inflammation
;  FILE REFERENCE: 99-108
;  CURRENT APPLICATION NUMBER: US/09/746,359A
;  CURRENT FILING DATE:  2001-05-21
;  PRIOR APPLICATION NUMBER: 60/171,969
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/213,341
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
;   LENGTH: 594
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-746-359A-23

  Query Match             95.1%;  Score 558;  DB 4;  Length 594;
  Best Local Similarity   95.5%;  Pred. No. 1.1e-57;
  Matches  105;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              ||    | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 APEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 437

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        438 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAK 487


RESULT 8
US-08-444-644-21
; Sequence 21, Application US/08444644
; Patent No. 6015555
;  GENERAL INFORMATION:
;    APPLICANT:  Friden, Phillip M.
;    TITLE OF INVENTION:  TRANSFERRIN RECEPTOR SPECIFIC
;    TITLE OF INVENTION:  ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
;    TITLE OF INVENTION:  CONJUGATES
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/444,644
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/232,246
;      FILING DATE:  07-JUL-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/800,458
;      FILING DATE:  26-NOV-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US90/05077
;      FILING DATE:  07-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/404,089
;      FILING DATE:  07-SEP-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wagner, Richard W.
;      REGISTRATION NUMBER:  34,480
;      REFERENCE/DOCKET NUMBER:  ALK88-15AAAZ
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  110 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-444-644-21

  Query Match             94.9%;  Score 557;  DB 3;  Length 110;
  Best Local Similarity   94.5%;  Pred. No. 1.5e-58;
  Matches  104;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||| ||: |||||||||
Db         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110


RESULT 9
US-08-232-246A-21
; Sequence 21, Application US/08232246A
; Patent No. 6329508
;  GENERAL INFORMATION:
;    APPLICANT:  Friden, Phillip M.
;    TITLE OF INVENTION:  TRANSFERRIN RECEPTOR SPECIFIC
```

```
;    TITLE OF INVENTION:  ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
;    TITLE OF INVENTION:  CONJUGATES
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,246A
;      FILING DATE:  04-MAY-1994
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/800,458
;      FILING DATE:  26-NOV-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US90/05077
;      FILING DATE:  07-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/404,089
;      FILING DATE:  07-SEP-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wagner, Richard W.
;      REGISTRATION NUMBER:  34,480
;      REFERENCE/DOCKET NUMBER:  ALK88-15AAA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  110 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-232-246A-21

  Query Match             94.9%;  Score 557;  DB 4;  Length 110;
  Best Local Similarity   94.5%;  Pred. No. 1.5e-58;
  Matches  104;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||| ||: |||||||||
Db         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110


RESULT 10
US-08-232-539D-55
; Sequence 55, Application US/08232539D
; Patent No. 5965709
;  GENERAL INFORMATION:
;    APPLICANT:  Presta, Leonard G.
;    APPLICANT:  Jardieu, Paula M.
;    TITLE OF INVENTION:  IgE Antagonists
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,539D
;      FILING DATE:  21-Apr-1994
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/178583
;      FILING DATE:  07-JAN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/744768
;      FILING DATE:  14-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Svoboda, Craig G.
;      REGISTRATION NUMBER:  39,044
;      REFERENCE/DOCKET NUMBER:  P0718P3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-1489
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  55:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  116 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-232-539D-55

  Query Match             94.9%;  Score 557;  DB 2;  Length 116;
  Best Local Similarity   94.5%;  Pred. No. 1.6e-58;
  Matches  104;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 65

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||| ||: |||||||||
Db         66 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 115


RESULT 11
US-08-430-633-4
; Sequence 4, Application US/08430633
; Patent No. 5726286
;  GENERAL INFORMATION:
;    APPLICANT:  ALDERSON, MARK
;    APPLICANT:  ARMITAGE, RICHARD
;    APPLICANT:  COHEN, JEFFREY
;    APPLICANT:  COMEAU, MICHAEL
;    APPLICANT:  FARRAH, THERESA
;    APPLICANT:  SPRIGGS, MELANIE
;    TITLE OF INVENTION:  Isolated Epstein-Barr Virus BZLF2 Proteins
;    TITLE OF INVENTION:  That Bind MHC Class II Beta Chains
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/430,633
;      FILING DATE:  28-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
```

```
;      APPLICATION NUMBER:  08/235,397
;      FILING DATE:  04/28/94
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia A.
;      REGISTRATION NUMBER:  34,693
;      REFERENCE/DOCKET NUMBER:  2612
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)233-0644
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  212 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  Human
;    IMMEDIATE SOURCE:
;      CLONE:  IgG1 Fc
US-08-430-633-4

  Query Match             94.9%;  Score 557;  DB 1;  Length 212;
  Best Local Similarity   94.5%;  Pred. No. 3.6e-58;
  Matches  104;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         14 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||| ||: |||||||||
Db         74 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 123


RESULT 12
US-08-620-694A-4
; Sequence 4, Application US/08620694A
; Patent No. 5869286
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 5869286el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/620,694A
;      FILING DATE:  21 MARCH 1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/538,765
;      FILING DATE:  7 AUGUST 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  212 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  Human
;    IMMEDIATE SOURCE:
;      CLONE:  IgG1 Fc
US-08-620-694A-4

  Query Match             94.9%;  Score 557;  DB 2;  Length 212;
  Best Local Similarity   94.5%;  Pred. No. 3.6e-58;
  Matches  104;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         14 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||| ||: |||||||||
Db         74 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 123


RESULT 13
US-08-936-854-4
; Sequence 4, Application US/08936854
; Patent No. 5925734
;  GENERAL INFORMATION:
;    APPLICANT:  ALDERSON, MARK
;    APPLICANT:  ARMITAGE, RICHARD
;    APPLICANT:  COHEN, JEFFREY
;    APPLICANT:  COMEAU, MICHAEL
;    APPLICANT:  FARRAH, THERESA
;    APPLICANT:  SPRIGGS, MELANIE
;    TITLE OF INVENTION:  Isolated Epstein-Barr Virus BZLF2 Proteins
;    TITLE OF INVENTION:  That Bind MHC Class II Beta Chains
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/936,854
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/430,633
;      FILING DATE:  28-APR-1995
;      APPLICATION NUMBER:  08/235,397
;      FILING DATE:  04/28/94
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia A.
;      REGISTRATION NUMBER:  34,693
;      REFERENCE/DOCKET NUMBER:  2612
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)233-0644
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  212 amino acids
```

```
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  Human
;    IMMEDIATE SOURCE:
;      CLONE:  IgG1 Fc
US-08-936-854-4

  Query Match             94.9%;  Score 557;  DB 2;  Length 212;
  Best Local Similarity   94.5%;  Pred. No. 3.6e-58;
  Matches  104;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         14 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||| ||: |||||||||
Db         74 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 123


RESULT 14
US-09-022-255-4
; Sequence 4, Application US/09022255
; Patent No. 6072033
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6072033el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/022,255
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/620,694
;      FILING DATE:  21 MARCH 1996
;      APPLICATION NUMBER:  USSN 08/538,765
;      FILING DATE:  7 AUGUST 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  212 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  Human
;    IMMEDIATE SOURCE:
;      CLONE:  IgG1 Fc
US-09-022-255-4

  Query Match             94.9%;  Score 557;  DB 3;  Length 212;
  Best Local Similarity   94.5%;  Pred. No. 3.6e-58;
  Matches  104;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         14 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||| ||: |||||||||
Db         74 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 123


RESULT 15
US-09-022-696-4
; Sequence 4, Application US/09022696
; Patent No. 6072037
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6072037el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/022,696
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/620,694
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  212 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  Human
;    IMMEDIATE SOURCE:
;      CLONE:  IgG1 Fc
US-09-022-696-4

  Query Match             94.9%;  Score 557;  DB 3;  Length 212;
  Best Local Similarity   94.5%;  Pred. No. 3.6e-58;
  Matches  104;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;
```

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         14 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73

Qy         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||||||||||||||||||||||||||||||||||| ||: ||||||||
Db         74 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 123
```

Search completed: April 29, 2004, 08:47:43
Job time : 17.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 29, 2004, 08:41:33 ; Search time 13.5 Seconds
(without alignments)
783.783 Million cell updates/sec

Title: US-09-674-857-12
Perfect score: 583
Sequence: 1 APPVAGGPSVFLFPPKPKDT.....CKVSNKGLPSSIEKTISKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	565	96.9	327	1	G4HU	Ig gamma-4 chain C
2	542.5	93.1	326	1	G2HU	Ig gamma-2 chain C
3	541	92.8	234	2	PT0207	Ig gamma chain C r
4	541	92.8	255	4	S31866	Ig gamma-1 chain C
5	541	92.8	330	1	GHHU	Ig gamma-1 chain C
6	541	92.8	374	2	S69339	Ig heavy chain V r
7	531	91.1	377	2	A60764	Ig gamma-3 chain C
8	531	91.1	377	2	A23511	Ig gamma-3 chain C
9	518	88.9	289	1	G3HUWI	Ig gamma-3 heavy c
10	470	80.6	328	2	I47160	Ig gamma 2b chain
11	470	80.6	328	2	I47159	Ig gamma 2a chain
12	465	79.8	277	2	I47162	Ig gamma 4 chain c
13	443	76.0	328	2	I47161	Ig gamma 3 chain c
14	443	76.0	328	2	I47158	Ig gamma 1 chain c
15	433	74.3	308	2	C30554	Ig heavy chain C r
16	433	74.3	323	1	GHRB	Ig gamma chain C r
17	433	74.3	333	2	PS0018	Ig gamma-2b chain
18	433	74.3	472	2	S31459	Ig gamma-1 chain -
19	431	73.9	470	2	S22080	Ig heavy chain pre
20	426	73.1	329	1	G2GP	Ig gamma-2 chain C
21	417	71.5	329	1	G3MSC	Ig gamma-3 chain C
22	417	71.5	398	1	G3MSM	Ig gamma-3 chain C
23	409	70.2	327	2	S06611	Ig gamma-2 chain C
24	405	69.5	324	1	G1MS	Ig gamma-1 chain C
25	405	69.5	393	1	G1MSM	Ig gamma-1 chain C
26	405	69.5	444	2	PC4436	monoclonal antibod
27	403	69.1	329	2	S00847	Ig gamma-2c chain
28	399	68.4	405	1	G2MSBM	Ig gamma-2b chain
29	399	68.4	474	1	G2MS11	Ig gamma-2b chain
30	396	67.9	335	1	G2MSAB	Ig gamma-2a chain
31	393	67.4	330	1	G2MSA	Ig gamma-2a chain
32	393	67.4	399	1	G2MSAM	Ig gamma-2a chain
33	393	67.4	469	2	S37483	Ig gamma-2a chain
34	389	66.7	326	2	PS0017	Ig gamma-1 chain C
35	385	66.0	475	2	S01321	Ig gamma-2b chain
36	383	65.7	446	2	S40295	Ig gamma-2a chain
37	343	58.8	322	2	PS0019	Ig gamma-2a chain
38	311	53.3	112	2	B30503	Ig gamma-2a chain
39	278	47.7	88	2	A30503	Ig gamma-2b chain
40	258	44.3	180	2	I46732	Ig gamma heavy cha
41	167.5	28.7	426	2	I36948	Ig epsilon-chain -
42	166.5	28.6	428	1	EHHU	Ig epsilon chain C
43	165	28.3	152	2	S14236	Ig gamma-1 chain C
44	154	26.4	549	2	S04845	Ig heavy chain pre
45	151	25.9	429	1	EHRT	Ig epsilon chain C

ALIGNMENTS

RESULT 1
G4HU
Ig gamma-4 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C;Accession: A90933; A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A;Reference number: A90933; MUID:83157104; PMID:6299662
A;Accession: A90933
A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Note: the sequence was determined from the germline gene
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant
A;Reference number: A90249; MUID:70207560; PMID:4192699
A;Accession: A90249
A;Molecule type: protein
A;Residues: 1-30;81-326 <PIN>
C;Genetics:
A;Gene: GDB:IGHG4
A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;99-110/Region: hinge
F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 96.9%; Score 565; DB 1; Length 327;
Best Local Similarity 97.3%; Pred. No. 1.2e-48;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 170

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 220
```

RESULT 2
G2HU
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A;Note: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constant region domains of a
A;Reference number: A90752; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A;Accession: A90752
A;Molecule type: protein
A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A;Reference number: A93132; MUID:80114419; PMID:118920
A;Contents: Zie
A;Accession: A93132
A;Molecule type: protein
A;Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidati
ned
R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG2
A;Cross-references: GDB:119338; OMIM:147110
A;Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;133-202/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,140-200,246-304/Disulfide bonds: #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 93.1%; Score 542.5; DB 1; Length 326;
Best Local Similarity 93.6%; Pred. No. 2.1e-46;
Matches 103; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||||| |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        111 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 169

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||:||||||||:|||||||||||||||||||||: ||||||| |
Db        170 PREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 219
```

RESULT 3
PT0207
Ig gamma chain C region - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C;Accession: PT0207
R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A;Reference number: PT0207; MUID:91287716; PMID:2062315
A;Accession: PT0207
A;Molecule type: mRNA
A;Residues: 1-234 <EHR>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;48-117/Domain: immunoglobulin homology <IMM>

Query Match 92.8%; Score 541; DB 2; Length 234;
Best Local Similarity 91.8%; Pred. No. 2e-46;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||| |||||:||||||||||||||||
Db         25 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 84

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||:|||||||||||||||||||||||||||||| ||: |||||||||
Db         85 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 134
```

RESULT 4
S31866
Ig gamma-1 chain C region - synthetic
C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
R;Filpula, D.
submitted to the EMBL Data Library, February 1993
A;Description: Screeing method for protein-protein interactions of cloned gene products
A;Reference number: S31866
A;Accession: S31866
A;Molecule type: mRNA
A;Residues: 1-255 <FIL>
A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C;Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region

Query Match 92.8%; Score 541; DB 4; Length 255;
Best Local Similarity 91.8%; Pred. No. 2.2e-46;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||| |||||:||||||||||||||||
Db         39 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 98

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||:|||||||||||||||||||||||||||||| ||: |||||||||
Db         99 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 148
```

RESULT 5
GHHU
Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432
A;Accession: A93433
A;Molecule type: DNA
A;Residues: 1-330 <ELL>
A;Cross-references: EMBL:Z17370
A;Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,
A;Note: Lys-330 is removed after translation
R;Harris, L.J.
submitted to the EMBL Data Library, October 1992
A;Reference number: S33904
A;Accession: S36861
A;Molecule type: DNA
A;Residues: 2-330 <HAR>
A;Cross-references: EMBL:Z17370
R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A;Reference number: S33887; MUID:83001943; PMID:6811139
A;Accession: S33887
A;Molecule type: DNA
A;Residues: 88-113;235-330 <TAK>
A;Cross-references: EMBL:Z17370
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
A;Reference number: A90563; MUID:71064024; PMID:5489771
A;Contents: myeloma protein Eu
A;Accession: B90563
A;Molecule type: protein
A;Residues: 1-96,'R',98-135 <CUN>
A;Note: this sequence has the G1m(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid seque
A;Reference number: A90564; MUID:71064025; PMID:5530842
A;Contents: Eu
A;Accession: A90564
A;Molecule type: protein
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,
A;Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met
R;Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
igen Primaerstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A;Note: this sequence has the G1m(17) and G1m(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A;Note: this sequence has the G1m(3) and G1m(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglo
enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match 92.8%; Score 541; DB 1; Length 330;
  Best Local Similarity 91.8%; Pred. No. 3e-46;
  Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||| |||||:||||||||||||||||
Db        114 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 173

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||:|||||||||||||||||||||||||||||||| ||: |||||||||
Db        174 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 223
```

RESULT 6
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: EMBL:X81695
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology

  Query Match 92.8%; Score 541; DB 2; Length 374;
  Best Local Similarity 91.8%; Pred. No. 3.5e-46;
  Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||||| |||||:||||||||||||||||
Db        158 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 217

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||:|||||||||||||||||||||||||||||||| ||: |||||||||
```

```
Db        218 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 267


RESULT 7
A60764
Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

  Query Match             91.1%;  Score 531;  DB 2;  Length 377;
  Best Local Similarity   90.0%;  Pred. No. 3.5e-45;
  Matches   99;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||| ||||||| ||||||||||||||
Db        161 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 220

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||:|||:|||||||||||||||||||||||| ||: ||||||| |
Db        221 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 270


RESULT 8
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: co
A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

  Query Match             91.1%;  Score 531;  DB 2;  Length 377;
  Best Local Similarity   90.0%;  Pred. No. 3.5e-45;
  Matches   99;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||| ||||||| ||||||||||||||
Db        161 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 220

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||:|||:|||||||||||||||||||||||| ||: ||||||| |
Db        221 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 270


RESULT 9
G3HUWI
Ig gamma-3 heavy chain disease proteins - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C;Accession: A90442; A92219; A90198; A93915; A02149
R;Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy
A;Reference number: A90442; MUID:81021548; PMID:6774747
A;Contents: heavy chain disease protein Wis
A;Accession: A90442
A;Molecule type: protein
A;Residues: 1-289 <FRA>
A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchai
A;Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 c
A;Note: the sequence of residues 42-76 was taken from the reference that follows
R;Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A;Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplicatic
A;Reference number: A92219; MUID:77118561; PMID:402363
A;Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein
A;Accession: A92219
A;Molecule type: protein
A;Residues: 12-97 <MIC>
A;Note: the hinge region in gamma-3 chains is about four times as long as in other gamm
idue segment (12-28)
A;Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inte
R;Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the
A;Reference number: A90198; MUID:77021516; PMID:823945
A;Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues
A;Accession: A90198
A;Molecule type: protein
A;Residues: 59-125,'EB',128-226,228-289 <WOL>
A;Note: this protein lacks most of the V region, all of the CH1 region, and part of the
R;Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A;Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion
A;Reference number: A93915; MUID:82247835; PMID:6808505
A;Contents: heavy chain disease protein Omm
A;Accession: A93915
A;Molecule type: mRNA
A;Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-15
A;Note: a carboxyl-terminal Lys is removed posttranslationally
A;Note: this sequence may represent an allelic form or another gamma chain subclass
C;Comment: The heavy chain disease protein Wis is shown.
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
F;203-270/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             88.9%;  Score 518;  DB 1;  Length 289;
  Best Local Similarity   87.3%;  Pred. No. 5e-44;
  Matches   96;  Conservative    7;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||| ||||||| |||||||:|||||||
Db         74 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVQVHNAKTK 133

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||:|||||:|||||||||:||:|||||||||| ||: ||||||| |
Db        134 PREQQFNSTFRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISKTK 183


RESULT 10
I47160
Ig gamma 2b chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
```

```
C;Accession: I47160
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C;Genetics:
A;Gene: IgG2b
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

  Query Match             80.6%;  Score 470;  DB 2;  Length 328;
  Best Local Similarity   81.7%;  Pred. No. 3.5e-39;
  Matches   85;  Conservative   12;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          7 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF 66
              ||||||:|||||||||||||||:||||||||||:|||||:|||||||||  |:|:|:||||
Db        116 GPSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQF 175

Qy         67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||| : |||||||||:|||:|| ||: | : |||||
Db        176 NSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAK 219


RESULT 11
I47159
Ig gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47159
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C;Genetics:
A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

  Query Match             80.6%;  Score 470;  DB 2;  Length 328;
  Best Local Similarity   81.7%;  Pred. No. 3.5e-39;
  Matches   85;  Conservative   12;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          7 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF 66
              ||||||:|||||||||||||||:||||||||||:|||||:|||||||||  |:|:|:||||
Db        116 GPSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQF 175

Qy         67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||| : |||||||||:|||:|| ||: | : |||||
Db        176 NSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAK 219


RESULT 12
I47162
Ig gamma 4 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47162
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47162
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-277 <KAC>
A;Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
C;Genetics:
A;Gene: IgG4
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>

  Query Match             79.8%;  Score 465;  DB 2;  Length 277;
  Best Local Similarity   80.8%;  Pred. No. 8.9e-39;
  Matches   84;  Conservative   12;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          7 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF 66
              ||| |:|||||||||||||||:||||||||||:|||||:|||||||||  |:|:|:||||
Db         65 GPSAFIFPPKPKDTLMISRTPKVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQF 124

Qy         67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||| : |||||||||:|||:|| ||: | : |||||
Db        125 NSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAK 168


RESULT 13
I47161
Ig gamma 3 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47161
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47161
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03781; NID:g433127; PIDN:AAA52219.1; PID:g433128
C;Genetics:
A;Gene: IgG3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

  Query Match             76.0%;  Score 443;  DB 2;  Length 328;
  Best Local Similarity   78.6%;  Pred. No. 1.7e-36;
  Matches   81;  Conservative   12;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          7 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF 66
              |||||:|||||||||||:|||||||||||:|  ||||:|||||||||  |:|:|:||||
Db        116 GPSVFIFPPKPKDTLMISQTPEVTCVVVDVSKEHAEVQFSWYVDGVEVHTAETRPKEEQF 175

Qy         67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKA 109
              |||||||||| : ||||| |||:||||:|  ||: | :|||||
Db        176 NSTYRVVSVLPIQHQDWLKGKEFKCKVNNVDLPAPITRTISKA 218


RESULT 14
I47158
Ig gamma 1 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47158
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47158
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122
C;Genetics:
A;Gene: IgG1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
```

Query Match 76.0%; Score 443; DB 2; Length 328;
Best Local Similarity 78.6%; Pred. No. 1.7e-36;
Matches 81; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

```
Qy          7 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF 66
              |||||:|||||||||||:|||||||||||:|  ||||:||||||| |:|:|:||||
Db        116 GPSVFIFPPKPKDTLMISQTPEVTCVVVDVSKEHAEVQFSWYVDGVEVHTAETRPKEEQF 175

Qy         67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKA 109
              |||||||||| : ||||| |||:||||:|  ||: | :|||||
Db        176 NSTYRVVSVLPIQHQDWLKGKEFKCKVNNVDLPAPITRTISKA 218
```

RESULT 15
C30554
Ig heavy chain C region - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
C;Accession: C30554
R;Foley, R.C.; Beh, K.J.
J. Immunol. 142, 708-711, 1989
A;Title: Isolation and sequence of sheep Ig H and L chain cDNA.
A;Reference number: A30554; MUID:89093962; PMID:2492052
A;Accession: C30554
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-308 <FOL>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;113-182/Domain: immunoglobulin homology <IMM>

Query Match 74.3%; Score 433; DB 2; Length 308;
Best Local Similarity 71.6%; Pred. No. 1.5e-35;
Matches 78; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

```
Qy          2 PPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 61
              | : ||||||:|||||||||| || |||||||||| |:||||||:|:|| ||| |:|||
Db         91 PELPGGPSVFIFPPKPKDTLTISGTPEVTCVVVDVGQDDPEVQFSWFVDNVEVRTARTKP 150

Qy         62 REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||:|||| | : ||||  |||:|||| |: ||: | :|||: |
Db        151 REEQFNSTFRVVSALPIQHQDWTGGKEFKCKVHNEALPAPIVRTISRTK 199
```

Search completed: April 29, 2004, 08:46:58
Job time : 14.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 29, 2004, 08:37:47 ; Search time 10 Seconds
(without alignments)
572.772 Million cell updates/sec

Title: US-09-674-857-12
Perfect score: 583
Sequence: 1 APPVAGGPSVFLFPPKPKDT.....CKVSNKGLPSSIEKTISKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	565	96.9	327	1	GC4_HUMAN	P01861 homo sapien
2	542.5	93.1	326	1	GC2_HUMAN	P01859 homo sapien
3	541	92.8	330	1	GC1_HUMAN	P01857 homo sapien
4	518	88.9	290	1	GC3_HUMAN	P01860 homo sapien
5	433	74.3	323	1	GC_RABIT	P01870 oryctolagus
6	433	74.3	333	1	GCB_RAT	P20761 rattus norv
7	426	73.1	329	1	GC2_CAVPO	P01862 cavia porce
8	417	71.5	329	1	GC3_MOUSE	P22436 mus musculu
9	417	71.5	398	1	GC3M_MOUSE	P03987 mus musculu
10	405	69.5	324	1	GC1_MOUSE	P01868 mus musculu
11	405	69.5	393	1	GC1M_MOUSE	P01869 mus musculu
12	403	69.1	329	1	GCC_RAT	P20762 rattus norv
13	399	68.4	336	1	GCB_MOUSE	P01866 mus musculu
14	399	68.4	405	1	GCBM_MOUSE	P01867 mus musculu
15	396	67.9	335	1	GCAB_MOUSE	P01864 mus musculu
16	393	67.4	330	1	GCAA_MOUSE	P01863 mus musculu
17	393	67.4	399	1	GCAM_MOUSE	P01865 mus musculu
18	389	66.7	326	1	GC1_RAT	P20759 rattus norv
19	343	58.8	322	1	GCA_RAT	P20760 rattus norv
20	166.5	28.6	428	1	EPC_HUMAN	P01854 homo sapien
21	151	25.9	429	1	EPC_RAT	P01855 rattus norv
22	151	25.9	457	1	MUC_SUNMU	P20768 suncus muri
23	140	24.0	421	1	EPC_MOUSE	P06336 mus musculu
24	138.5	23.8	299	1	ALC_RABIT	P01879 oryctolagus
25	138	23.7	454	1	MUC_HUMAN	P01871 homo sapien
26	136	23.3	391	1	MUCB_HUMAN	P04220 homo sapien
27	133	22.8	106	1	KAC_HUMAN	P01834 homo sapien
28	132	22.6	454	1	MUC_MESAU	P06337 mesocricetu
29	132	22.6	455	1	MUC_MOUSE	P01872 mus musculu
30	132	22.6	476	1	MUCM_MOUSE	P01873 mus musculu
31	128	22.0	103	1	LAC_CHICK	P20763 gallus gall
32	125	21.4	450	1	MUC_CANFA	P01874 canis famil
33	125	21.4	458	1	MUC_RABIT	P03988 oryctolagus
34	125	21.4	479	1	MUCM_RABIT	P04221 oryctolagus
35	122.5	21.0	105	1	LAC5_MUSSP	P20765 mus spretus
36	120.5	20.7	105	1	LAC1_MOUSE	P01843 mus musculu
37	120.5	20.7	340	1	ALC2_HUMAN	P01877 homo sapien
38	120.5	20.7	353	1	ALC1_GORGO	P20758 gorilla gor
39	120.5	20.7	353	1	ALC1_HUMAN	P01876 homo sapien
40	119.5	20.5	105	1	LAC5_MOUSE	P20764 mus musculu
41	114	19.6	103	1	KAC4_RABIT	P01840 oryctolagus
42	111.5	19.1	344	1	ALC_MOUSE	P01878 mus musculu
43	111.5	19.1	393	1	HVC3_HETFR	P23086 heterodontu
44	110.5	19.0	213	1	ILL1_HUMAN	P15814 homo sapien
45	109.5	18.8	105	1	LAC_HUMAN	P01842 homo sapien

ALIGNMENTS

```
RESULT 1
GC4_HUMAN
ID   GC4_HUMAN      STANDARD;      PRT;   327 AA.
AC   P01861;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig gamma-4 chain C region.
GN   IGHG4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83157104; PubMed=6299662;
RA   Ellison J.W., Buxbaum J.N., Hood L.E.;
RT   "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL   DNA 1:11-18(1981).
RN   [2]
RP   SEQUENCE OF 1-30 AND 81-326.
RX   MEDLINE=70207560; PubMed=4192699;
RA   Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT   "Human immunoglobulin subclasses. Partial amino acid sequence of the
RT   constant region of a gamma 4 chain.";
RL   Biochem. J. 117:33-47(1970).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; K01316; AAB59394.1; ALT_INIT.
DR   PIR; A90933; G4HU.
DR   PDB; 1ADQ; 16-SEP-98.
DR   Genew; HGNC:5528; IGHG4.
DR   MIM; 147130; -.
DR   GO; GO:0005624; C:membrane fraction; NAS.
DR   GO; GO:0003823; F:antigen binding; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT   NON_TER       1      1
FT   DOMAIN        1     98       CH1.
FT   DOMAIN       99    110       HINGE.
FT   DOMAIN      111    220       CH2.
FT   DOMAIN      221    327       CH3.
```

```
FT   DISULFID     14     14       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     83
FT   DISULFID    106    106       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    141    201
FT   DISULFID    247    305
SQ   SEQUENCE   327 AA;  35940 MW;  3EDBD811EF208E7A CRC64;

  Query Match             96.9%;  Score 565;  DB 1;  Length 327;
  Best Local Similarity   97.3%;  Pred. No. 1.3e-50;
  Matches  107;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 170

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 220


RESULT 2
GC2_HUMAN
ID   GC2_HUMAN      STANDARD;      PRT;   326 AA.
AC   P01859;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig gamma-2 chain C region.
GN   IGHG2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE OF 2-326 FROM N.A.
RX   MEDLINE=82197621; PubMed=6804948;
RA   Ellison J.W., Hood L.E.;
RT   "Linkage and sequence homology of two human immunoglobulin gamma
RT   heavy chain constant region genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN   [2]
RP   SEQUENCE OF 88-115 FROM N.A.
RC   TISSUE=Fetal liver;
RX   MEDLINE=83001943; PubMed=6811139;
RA   Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
RT   "Structure of human immunoglobulin gamma genes: implications for
RT   evolution of a gene family.";
RL   Cell 29:671-679(1982).
RN   [3]
RP   SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RC   TISSUE=Fetal liver;
RX   MEDLINE=84235992; PubMed=6329676;
RA   Krawinkel U., Rabbitts T.H.;
RT   "Comparison of the hinge-coding segments in human immunoglobulin gamma
RT   heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
RT   genes.";
RL   EMBO J. 1:403-407(1982).
RN   [4]
RP   SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX   MEDLINE=81007873; PubMed=6774012;
RA   Wang A.-C., Tung E., Fudenberg H.H.;
RT   "The primary structure of a human IgG2 heavy chain: genetic,
RT   evolutionary, and functional implications.";
RL   J. Immunol. 125:1048-1054(1980).
RN   [5]
RP   SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX   MEDLINE=80001357; PubMed=113060;
RA   Connell G.E., Parr D.M., Hofmann T.;
RT   "The amino acid sequences of the three heavy chain constant region
RT   domains of a human IgG2 myeloma protein.";
RL   Can. J. Biochem. 57:758-767(1979).
RN   [6]
RP   SEQUENCE OF 238-275 (ZIE).
RX   MEDLINE=80114419; PubMed=118920;
RA   Hofmann T., Parr D.M.;
RT   "A note of the amino acid sequence of residues 381-391 of human
RT   immunoglobulins gamma chains.";
RL   Mol. Immunol. 16:923-925(1979).
RN   [7]
RP   REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RA   Hofmann T., Parr D.M.;
RL   Submitted (MAR-1980) to the PIR data bank.
RN   [8]
RP   SEQUENCE OF 1-121 (DOT).
RX   MEDLINE=95255298; PubMed=7737190;
RA   Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT   "Characterization of the two unique human anti-flavin monoclonal
RT   immunoglobulins.";
RL   Eur. J. Biochem. 228:886-893(1995).
RN   [9]
RP   DISULFIDE BONDS.
RX   MEDLINE=72033500; PubMed=4940472;
RA   Milstein C., Frangione B.;
RT   "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RL   Biochem. J. 121:217-225(1971).
RN   [10]
RP   DISULFIDE BONDS.
RX   MEDLINE=69064124; PubMed=5782707;
RA   Frangione B., Milstein C., Pink J.R.L.;
RT   "Structural studies of immunoglobulin G.";
RL   Nature 221:145-148(1969).
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; J00230; AAB59393.1; -.
DR   PIR; A93906; G2HU.
DR   HSSP; P01857; 1FC1.
DR   Genew; HGNC:5526; IGHG2.
DR   MIM; 147110; -.
DR   GO; GO:0005624; C:membrane fraction; NAS.
DR   GO; GO:0003823; F:antigen binding; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Immunoglobulin domain; Immunoglobulin C region.
FT   NON_TER       1      1
FT   DOMAIN        1     98       CH1.
FT   DOMAIN       99    110       HINGE.
FT   DOMAIN      111    219       CH2.
FT   DOMAIN      220    326       CH3.
FT   DISULFID     14     14       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     83
FT   DISULFID    102    102       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    103    103       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    106    106       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    140    200
FT   DISULFID    246    304
FT   SITE        156    156       AT OR NEAR THE COMPLEMENT-BINDING SITE.
FT   MOD_RES     326    326       REMOVED POST-TRANSLATIONALLY (PROBABLE).
FT   VARIANT      60     60       S -> A (IN MYELOMA PROTEINS TIL & ZIE).
FT                                /FTId=VAR_003889.
FT   CONFLICT    109    109       C -> S (IN REF. 3).
SQ   SEQUENCE   326 AA;  35884 MW;  8310878C6878CF9C CRC64;
```

```
  Query Match             93.1%;  Score 542.5;  DB 1;  Length 326;
  Best Local Similarity   93.6%;  Pred. No. 2.7e-48;
  Matches  103;  Conservative    3;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||||| |||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db        111 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 169

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||:|||||||||:|||||||||||||||||||: ||||||| |
Db        170 PREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 219


RESULT 3
GC1_HUMAN
ID   GC1_HUMAN      STANDARD;      PRT;   330 AA.
AC   P01857;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ig gamma-1 chain C region.
GN   IGHG1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82274238; PubMed=6287432;
RA   Ellison J.W., Berson B.J., Hood L.E.;
RT   "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL   Nucleic Acids Res. 10:4071-4079(1982).
RN   [2]
RP   SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX   MEDLINE=71064024; PubMed=5489771;
RA   Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA   Waxdal M.J., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT   acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL   Biochemistry 9:3161-3170(1970).
RN   [3]
RP   SEQUENCE OF 136-329 (EU).
RX   MEDLINE=71064025; PubMed=5530842;
RA   Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA   Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT   acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL   Biochemistry 9:3171-3181(1970).
RN   [4]
RP   SEQUENCE (MYELOMA PROTEIN NIE).
RX   MEDLINE=77070269; PubMed=826475;
RA   Ponstingl H., Hilschmann N.;
RT   "The rule of antibody structure. The primary structure of a
RT   monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The
RT   chymotryptic peptides of the H-chain, alignment of the tryptic
RT   peptides and discussion of the complete structure.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN   [5]
RP   SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX   MEDLINE=83289131; PubMed=6884994;
RA   Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT   "Three-dimensional structure determination of antibodies. Primary
RT   structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN   [6]
RP   DISULFIDE BONDS.
RX   MEDLINE=71064027; PubMed=4923144;
RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
RT   Intrachain disulfide bonds.";
RL   Biochemistry 9:3188-3196(1970).
RN   [7]
RP   DISULFIDE BONDS.
RX   MEDLINE=77070267; PubMed=1002129;
RA   Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
RT   characterization of the protein, the L- and H-chains, the
RT   cyanogen bromide cleavage products, and the disulfide bridges.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX   MEDLINE=81208100; PubMed=7236608;
RA   Deisenhofer J.;
RT   "Crystallographic refinement and atomic models of a human Fc fragment
RT   and its complex with fragment B of protein A from Staphylococcus
RT   aureus at 2.9- and 2.8-A resolution.";
RL   Biochemistry 20:2361-2370(1981).
CC   -!- MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and the
CC       G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the
CC       G1M(3) marker and the G1M (non-1) markers.
CC   -!- MISCELLANEOUS: Nie also differs in the amidation states of
CC       35, 116, 198, 269 and 272.
CC   -!- MISCELLANEOUS: EU also differs in the amidation states of residues
CC       155, 166, 177, 195, 198, 269, and 272 and in the order of residues
CC       268-272.
CC   -!- MISCELLANEOUS: KOL also differs in the amidation states of
CC       residues 198, 267 and 272.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; J00228; AAC82527.1; ALT_INIT.
DR   PIR; A93433; GHHU.
DR   PDB; 1FC1; 15-JUL-92.
DR   PDB; 1FC2; 15-JUL-92.
DR   PDB; 1AJ7; 12-NOV-97.
DR   PDB; 1D5B; 09-FEB-00.
DR   PDB; 1D5I; 09-FEB-00.
DR   PDB; 1D6V; 04-OCT-00.
DR   PDB; 1DN2; 17-MAY-00.
DR   PDB; 1E4K; 06-JUN-01.
DR   PDB; 1FCC; 20-JUL-95.
DR   PDB; 1HZH; 12-JUN-02.
DR   PDB; 1I7Z; 08-AUG-01.
DR   PDB; 1IIS; 16-MAY-01.
DR   PDB; 1IIX; 16-MAY-01.
DR   PDB; 1L6X; 10-APR-02.
DR   PDB; 2RCS; 12-NOV-97.
DR   Genew; HGNC:5525; IGHG1.
DR   MIM; 147100; -.
DR   GO; GO:0005624; C:membrane fraction; NAS.
DR   GO; GO:0003823; F:antigen binding; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   3D-structure.
FT   NON_TER       1      1
FT   DOMAIN        1     98       CH1.
FT   DOMAIN       99    110       HINGE.
FT   DOMAIN      111    223       CH2.
FT   DOMAIN      224    330       CH3.
FT   DISULFID     27     83
FT   DISULFID    103    103       INTERCHAIN (WITH LIGHT CHAIN).
```

```
FT   DISULFID    109    109       INTERCHAIN (WITH HEAVY CHAIN).
FT   DISULFID    112    112       INTERCHAIN (WITH HEAVY CHAIN).
FT   DISULFID    144    204
FT   DISULFID    250    308
FT   CARBOHYD    180    180       N-LINKED (GLCNAC. . .).
FT   MOD_RES     330    330       REMOVED POST-TRANSLATIONALLY.
FT   VARIANT      97     97       K -> R (IN G1M(3) MARKER).
FT                                /FTId=VAR_003886.
FT   VARIANT     239    239       D -> E (IN G1M(NON-1) MARKER).
FT                                /FTId=VAR_003887.
FT   VARIANT     241    241       L -> M (IN G1M(NON-1) MARKER).
FT                                /FTId=VAR_003888.
FT   STRAND      122    126
FT   HELIX       130    134
FT   TURN        136    137
FT   STRAND      141    147
FT   STRAND      157    162
FT   TURN        163    164
FT   STRAND      165    166
FT   TURN        168    171
FT   STRAND      176    179
FT   TURN        180    181
FT   STRAND      182    190
FT   HELIX       193    197
FT   TURN        198    199
FT   STRAND      202    207
FT   TURN        209    210
FT   STRAND      215    219
FT   STRAND      227    227
FT   STRAND      230    234
FT   HELIX       238    242
FT   STRAND      245    256
FT   STRAND      260    265
FT   STRAND      270    270
FT   STRAND      274    276
FT   STRAND      280    281
FT   TURN        283    284
FT   STRAND      287    296
FT   HELIX       297    301
FT   TURN        302    303
FT   STRAND      305    312
FT   TURN        313    314
FT   TURN        316    317
FT   STRAND      320    325
SQ   SEQUENCE   330 AA;  36106 MW;  3770EE106C2FA33D CRC64;

  Query Match             92.8%;  Score 541;  DB 1;  Length 330;
  Best Local Similarity   91.8%;  Pred. No. 3.9e-48;
  Matches  101;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||||| |||||:||||||||||||||||
Db        114 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 173

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||:|||||||||||||||||||||||||||||| ||: |||||||||
Db        174 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 223


RESULT 4
GC3_HUMAN
ID   GC3_HUMAN      STANDARD;      PRT;   290 AA.
AC   P01860;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
GN   IGHG3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE (DISEASE PROTEIN WIS).
RX   MEDLINE=81021548; PubMed=6774747;
RA   Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
RT   "Primary structure of human gamma 3 immunoglobulin deletion mutant:
RT   gamma 3 heavy-chain disease protein Wis.";
RL   Biochemistry 19:4304-4308(1980).
RN   [2]
RP   REVISIONS TO 12-97 (PROTEIN WIS).
RX   MEDLINE=77118561; PubMed=402363;
RA   Michaelsen T.E., Frangione B., Franklin E.C.;
RT   "Primary structure of the 'hinge' region of human IgG3. Probable
RT   quadruplication of a 15-amino acid residue basic unit.";
RL   J. Biol. Chem. 252:883-889(1977).
RN   [3]
RP   REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).
RX   MEDLINE=77021516; PubMed=823945;
RA   Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
RT   "The amino acid sequence of 'heavy chain disease' protein ZUC.
RT   Structure of the Fc fragment of immunoglobulin G3.";
RL   Biochem. Biophys. Res. Commun. 71:907-914(1976).
RN   [4]
RP   SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RX   MEDLINE=82247835; PubMed=6808505;
RA   Alexander A., Steinmetz M., Barritault D., Frangione B.,
RA   Franklin E.C., Hood L., Buxbaum J.N.;
RT   "Gamma Heavy chain disease in man: cDNA sequence supports partial
RT   gene deletion model.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
CC   -!- SUBUNIT: Dimer linked by 12 disulfide bonds; it has an extra
CC       interchain disulfide bond at position 7 in addition to the 11
CC       normally present in the hinge region.
CC   -!- MISCELLANEOUS: The heavy chain disease protein WIS is shown.
CC   -!- MISCELLANEOUS: The sequence of residues 42-76 was taken from the
CC       Ref.2.
CC   -!- MISCELLANEOUS: Disease protein WIS is lacking most of the V region
CC       and all of the CH1 region.
CC   -!- MISCELLANEOUS: Disease protein ZUC lack most of the V region, all
CC       of the CH1 region, and part of the hinge compared with normal
CC       gamma-3 heavy chains.
CC   -!- MISCELLANEOUS: Disease protein OMM may represent an allelic form
CC       or another gamma chain subclass.
CC   -!- MISCELLANEOUS: The hinge region in gamma-3 chains is about four
CC       times as long as in other gamma chains and contains three
CC       identical 15-residue segments preceded by a similar 17-residue
CC       segment (12-28).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00231; AAA52805.1; ALT_SEQ.
DR   HSSP; P01857; 1FC1.
DR   Genew; HGNC:5527; IGHG3.
DR   MIM; 147120; -.
DR   GO; GO:0005624; C:membrane fraction; NAS.
DR   GO; GO:0003823; F:antigen binding; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat;
KW   Pyrrolidone carboxylic acid.
FT   DOMAIN       12     73       HINGE.
FT   DOMAIN       74    183       CH2.
FT   DOMAIN      184    289       CH3.
```

```
FT   REPEAT        29      43
FT   REPEAT        44      58
FT   REPEAT        59      73
FT   MOD_RES        1       1       PYRROLIDONE CARBOXYLIC ACID.
FT   CARBOHYD       6       6       N-LINKED (GLCNAC. . .).
FT   DISULFID       7       7       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID      24      24       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID      27      27       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID      33      33       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID      39      39       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID      42      42       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID      48      48       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID      54      54       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID      57      57       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID      63      63       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID      69      69       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID      72      72       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   CARBOHYD     140     140       N-LINKED (GLCNAC. . .).
FT   MOD_RES      290     290       REMOVED POST-TRANSLATIONALLY.
FT   VARIANT      126     127       QV -> EB (IN ZUC).
FT                                  /FTId=VAR_003890.
FT   VARIANT      134     134       P -> L (IN OMM).
FT                                  /FTId=VAR_003891.
FT   VARIANT      139     139       F -> Y (IN OMM).
FT                                  /FTId=VAR_003892.
FT   VARIANT      182     182       T -> A (IN OMM).
FT                                  /FTId=VAR_003893.
FT   VARIANT      227     227       S -> N (IN OMM).
FT                                  /FTId=VAR_003894.
FT   VARIANT      227     227       MISSING (IN ZUC).
FT                                  /FTId=VAR_003895.
FT   VARIANT      279     279       F -> Y (IN OMM).
FT                                  /FTId=VAR_003896.
SQ   SEQUENCE   290 AA;  32331 MW;  B69CBC95705B2F46 CRC64;

  Query Match             88.9%;  Score 518;  DB 1;  Length 290;
  Best Local Similarity   87.3%;  Pred. No. 7.7e-46;
  Matches   96;  Conservative    7;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||| ||||||| ||||||:|||||||
Db         74 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVQVHNAKTK 133

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||:|||||:|||||||||||:||:|||||||||||  ||: |||||||
Db        134 PREQQFNSTFRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISKTK 183


RESULT 5
GC_RABIT
ID   GC_RABIT       STANDARD;      PRT;   323 AA.
AC   P01870;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig gamma chain C region.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84030930; PubMed=6313520;
RA   Bernstein K.E., Alexander C.B., Mage R.G.;
RT   "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
RT   F-I haplotype.";
RL   Immunogenetics 18:387-397(1983).
RN   [2]
RP   SEQUENCE OF 1-128.
RX   MEDLINE=76135469; PubMed=1243651;
RA   Pratt D.M., Mole L.E.;
RT   "Sequence studies on the constant region of the Fd sections of rabbit
RT   immunoglobulin G of different allotype.";
RL   Biochem. J. 151:337-349(1975).
RN   [3]
RP   SEQUENCE OF 88-266 FROM N.A.
RX   MEDLINE=83299917; PubMed=6193512;
RA   Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT   "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
RT   heavy chain and identification of two genomic C gamma genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN   [4]
RP   SEQUENCE OF 132-161.
RX   MEDLINE=70110015; PubMed=5461106;
RA   Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT   "Sequence studies of the Fd section of the heavy chain of rabbit
RT   immunoglobulin G.";
RL   Biochem. J. 116:249-259(1970).
RN   [5]
RP   SEQUENCE OF 129-131 AND 155-322.
RA   Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
RL   (In) Killander J. (eds.);
RL   Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
RL   Stockholm (1967).
CC   -!- MISCELLANEOUS: Ref.1 sequence has the D12 allotypic marker,
CC       104-Thr, and the E14 marker, 185-Thr. Ref.3 has the D11 and E15
CC       markers and Ref.5 the E15 marker.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M16426; AAA31289.1; -.
DR   PIR; A91749; GHRB.
DR   HSSP; P01857; 1FC1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Repeat.
FT   NON_TER       1       1
FT   DOMAIN        6      96       IG-LIKE 1.
FT   DOMAIN      114     213       IG-LIKE 2.
FT   DOMAIN      222     318       IG-LIKE 3.
FT   VARIANT     104     104       T -> M (IN D11 MARKER).
FT   VARIANT     185     185       T -> A (IN E15 MARKER).
FT   CONFLICT     48      48       N -> E (IN REF. 2).
FT   CONFLICT     71      71       V -> VPV (IN REF. 2).
FT   CONFLICT    144     144       Q -> E (IN REF. 3 AND 4).
FT   CONFLICT    173     173       N -> D (IN REF. 5).
FT   CONFLICT    187     187       Q -> E (IN REF. 3 AND 5).
FT   CONFLICT    201     201       N -> D (IN REF. 5).
FT   CONFLICT    218     218       Q -> E (IN REF. 5).
FT   CONFLICT    233     233       E -> Q (IN REF. 5).
FT   CONFLICT    246     246       N -> D (IN REF. 5).
FT   CONFLICT    256     256       E -> G (IN REF. 5).
FT   CONFLICT    260     260       N -> D (IN REF. 5).
FT   CONFLICT    266     266       N -> D (IN REF. 5).
FT   CONFLICT    280     280       Y -> W (IN REF. 5).
FT   CONFLICT    284     284       N -> S (IN REF. 5).
SQ   SEQUENCE   323 AA;  35404 MW;  69E8AA118D579A8B CRC64;

  Query Match             74.3%;  Score 433;  DB 1;  Length 323;
  Best Local Similarity   72.5%;  Pred. No. 4.6e-37;
  Matches   79;  Conservative   12;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          2 PPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 61
              | : |||||||:|||||||||||||||||||||||||||:|||||| ||::  :|  |:
```

```
Db        108 PELLGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTARPPL 167

Qy         62 REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||:||||| |||| | : ||||| |||:|||| || ||: ||||||||:
Db        168 REQQFNSTIRVVSTLPITHQDWLRGKEFKCKVHNKALPAPIEKTISKAR 216


RESULT 6
GCB_RAT
ID   GCB_RAT        STANDARD;      PRT;   333 AA.
AC   P20761;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig gamma-2B chain C region.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89232738; PubMed=3149946;
RA   Brueggemann M.;
RT   "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL   Gene 74:473-482(1988).
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
DR   PIR; PS0018; PS0018.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Repeat.
FT   NON_TER       1      1
FT   DOMAIN        6     96       IG-LIKE 1.
FT   DOMAIN      124    223       IG-LIKE 2.
FT   DOMAIN      232    328       IG-LIKE 3.
FT   DISULFID     15     15       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     80
FT   DISULFID    106    106       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    112    112       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    115    115       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    147    207
FT   DISULFID    253    311
SQ   SEQUENCE   333 AA;  36497 MW;  55F8B64D48D460A6 CRC64;

  Query Match             74.3%;  Score 433;  DB 1;  Length 333;
  Best Local Similarity   69.7%;  Pred. No. 4.7e-37;
  Matches   76;  Conservative   20;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          2 PPVAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 61
              | : ||||||:|||||||  |:||:  :||||||||||:|:|:|||:|:|: |||| |:|:|
Db        118 PELLGGPSVFIPPPKPKDILLISQNAKVTCVVVDVSEEEPDVQFSWFVNNVEVHTAQTQP 177

Qy         62 REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||:|||:|||| | : |||::|||:||||:|| ||| |||||||| |
Db        178 REEQYNSTFRVVSALPIQHQDWMSGKEFKCKVNNKALPSPIEKTISKPK 226


RESULT 7
GC2_CAVPO
ID   GC2_CAVPO      STANDARD;      PRT;   329 AA.
AC   P01862;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig gamma-2 chain C region.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE OF 1-3.
RA   Trischmann T.M.;
RL   Submitted (APR-1975) to the PIR data bank.
RN   [2]
RP   SEQUENCE OF 4-68.
RX   MEDLINE=71058471; PubMed=5538606;
RA   Birshtein B.K., Hussain Q.Z., Cebra J.J.;
RT   "Structure of heavy chain from strain 13 guinea pig
RT   immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT   half-cystine joining heavy and light chains.";
RL   Biochemistry 10:18-25(1971).
RN   [3]
RP   SEQUENCE OF 69-133 AND 312-329.
RX   MEDLINE=71058486; PubMed=5538616;
RA   Turner K.J., Cebra J.J.;
RT   "Structure of heavy chain from strain 13 guinea pig
RT   immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT   and hinge region cyanogen bromide fragments.";
RL   Biochemistry 10:9-17(1971).
RN   [4]
RP   SEQUENCE OF 134-226.
RX   MEDLINE=75036072; PubMed=4429665;
RA   Tracey D.E., Cebra J.J.;
RT   "Primary structure of the CH2 homology region from guinea pig IgG2
RT   antibodies.";
RL   Biochemistry 13:4796-4803(1974).
RN   [5]
RP   SEQUENCE OF 227-311.
RX   MEDLINE=75036073; PubMed=4609467;
RA   Trischmann T.M., Cebra J.J.;
RT   "Primary structure of the CH3 homology region from guinea pig IgG2
RT   antibodies.";
RL   Biochemistry 13:4804-4811(1974).
RN   [6]
RP   DISULFIDE BONDS.
RX   MEDLINE=71058474; PubMed=4922544;
RA   Oliveira B., Lamm M.E.;
RT   "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL   Biochemistry 10:26-31(1971).
CC   -!- MISCELLANEOUS: This chain was isolated from pooled serum of strain
CC       13 inbred guinea pigs.
DR   PIR; A94553; G2GP.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT   NON_TER       1      1
FT   DISULFID     16     16       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     28     79
FT   DISULFID    105    105       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    107    107       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    110    110       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    142    202
FT   CARBOHYD    178    178       N-LINKED (GLCNAC. . .).
FT   DISULFID    248    308
SQ   SEQUENCE   329 AA;  36074 MW;  5D231B7164D1FBA9 CRC64;

  Query Match             73.1%;  Score 426;  DB 1;  Length 329;
  Best Local Similarity   72.5%;  Pred. No. 2.4e-36;
  Matches   79;  Conservative   11;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          2 PPVAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 61
              |   ||||||:|||||||||||| || ||||||||||::|||||  |:||   | ||:|||
Db        113 PENLGGPSVFIFPPKPKDTLMISLTPRVTCVVVDVSQDEPEVQFTWFVDNKPVGNAETKP 172
```

```
Qy         62 REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              | ||:|:|:|| ||| : ||||| |||:|||| || ||: ||||||| |
Db        173 RVEQYNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKTK 221


RESULT 8
GC3_MOUSE
ID   GC3_MOUSE      STANDARD;      PRT;   329 AA.
AC   P22436;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig gamma-3 chain C region, secreted form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85027161; PubMed=6092053;
RA   Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA   Tucker P.W., Blattner F.R.;
RT   "Structural analysis of the murine IgG3 constant region gene.";
RL   EMBO J. 3:2041-2046(1984).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00451; -; NOT_ANNOTATED_CDS.
DR   PIR; B02156; G3MSC.
DR   HSSP; P01857; 1FC1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Transmembrane; Alternative splicing.
FT   NON_TER       1      1
FT   DOMAIN        1     97       CH1.
FT   DOMAIN       98    113       HINGE.
FT   DOMAIN      114    223       CH2.
FT   DOMAIN      224    327       CH3.
SQ   SEQUENCE   329 AA;  36228 MW;  F45827174182BAD6 CRC64;

  Query Match             71.5%;  Score 417;  DB 1;  Length 329;
  Best Local Similarity   67.6%;  Pred. No. 2e-35;
  Matches   75;  Conservative   17;  Mismatches   17;  Indels    2;  Gaps    1;

Qy          2 PP--VAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKT 59
              ||  : |||||||:||||||| |||| ||:|||||||||::||:|  :|:||  ||| | |
Db        112 PPGNILGGPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWT 171

Qy         60 KPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              :||| |:|||:|||| | : |||| |||:||||:|| ||: ||:|||| |
Db        172 QPREAQYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPK 222


RESULT 9
GC3M_MOUSE
ID   GC3M_MOUSE     STANDARD;      PRT;   398 AA.
AC   P03987;
DT   23-OCT-1986 (Rel. 02, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig gamma-3 chain C region, membrane-bound form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85027161; PubMed=6092053;
RA   Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA   Tucker P.W., Blattner F.R.;
RT   "Structural analysis of the murine IgG3 constant region gene.";
RL   EMBO J. 3:2041-2046(1984).
RN   [2]
RP   SEQUENCE OF 328-398 FROM N.A.
RX   MEDLINE=84041483; PubMed=6314258;
RA   Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA   Wall R.;
RT   "The structure of the mouse immunoglobulin in gamma 3 membrane gene
RT   segment.";
RL   Nucleic Acids Res. 11:6775-6785(1983).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00451; AAB59655.1; -.
DR   EMBL; V01526; CAA24767.1; ALT_SEQ.
DR   PIR; A02156; G3MSM.
DR   HSSP; P01857; 1FC1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Transmembrane; Alternative splicing.
FT   NON_TER       1      1
FT   DOMAIN        1     97       CH1.
FT   DOMAIN       98    113       HINGE.
FT   DOMAIN      114    223       CH2.
FT   DOMAIN      224    327       CH3.
FT   TRANSMEM    346    362       POTENTIAL.
FT   DOMAIN      363    398       CYTOPLASMIC (POTENTIAL).
FT   CONFLICT    333    333       E -> G (IN REF. 2).
FT   CONFLICT    342    342       E -> Q (IN REF. 2).
FT   CONFLICT    388    388       P -> F (IN REF. 2).
SQ   SEQUENCE   398 AA;  43929 MW;  CF7F264B50A41B95 CRC64;

  Query Match             71.5%;  Score 417;  DB 1;  Length 398;
  Best Local Similarity   67.6%;  Pred. No. 2.6e-35;
  Matches   75;  Conservative   17;  Mismatches   17;  Indels    2;  Gaps    1;

Qy          2 PP--VAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKT 59
              ||  : |||||||:||||||| |||| ||:|||||||||::||:|  :|:||  ||| | |
Db        112 PPGNILGGPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWT 171

Qy         60 KPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              :||| |:|||:|||| | : |||| |||:||||:|| ||: ||:|||| |
Db        172 QPREAQYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPK 222


RESULT 10
GC1_MOUSE
ID   GC1_MOUSE      STANDARD;      PRT;   324 AA.
AC   P01868;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
```

```
DE   Ig gamma-1 chain C region secreted form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=80045036; PubMed=115593;
RA   Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA   Takahashi N., Mano Y.;
RT   "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT   gamma 1 chain gene.";
RL   Cell 18:559-568(1979).
RN   [2]
RP   SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX   MEDLINE=80202559; PubMed=6769752;
RA   Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA   Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT   "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
RT   cloned in a bacterial plasmid.";
RL   Gene 9:87-97(1980).
RN   [3]
RP   SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX   MEDLINE=80012837; PubMed=113776;
RA   Rogers J., Clarke P., Salser W.;
RT   "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
RT   heavy chain.";
RL   Nucleic Acids Res. 6:3305-3321(1979).
RN   [4]
RP   SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX   MEDLINE=78242288; PubMed=98524;
RA   Adetugbo K.;
RT   "Evolution of immunoglobulin subclasses. Primary structure of a
RT   murine myeloma gammal chain.";
RL   J. Biol. Chem. 253:6068-6075(1978).
RN   [5]
RP   DISULFIDE BONDS (MOPC 21).
RX   MEDLINE=73008889; PubMed=5073237;
RA   Svasti J., Milstein C.;
RT   "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL   Biochem. J. 126:837-850(1972).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Secreted;
CC         IsoId=P01868-1; Sequence=Displayed;
CC         Note=May be the major isoform;
CC       Name=Membrane-bound;
CC         IsoId=P01869-1; Sequence=External;
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; V00793; CAA24172.1; -.
DR   EMBL; V00793; CAA24173.1; -.
DR   EMBL; V00793; CAA24174.1; -.
DR   EMBL; V00793; CAA24175.1; -.
DR   EMBL; V00795; CAA24176.1; -.
DR   PIR; A02159; G1MS.
DR   GlycoSuiteDB; P01868; -.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Alternative splicing.
FT   NON_TER       1      1
FT   DOMAIN        1     97       CH1.
FT   DOMAIN       98    110       HINGE.
FT   DOMAIN      111    217       CH2.
FT   DOMAIN      218    324       CH3.
FT   DISULFID     27     82
FT   DISULFID    102    102       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID    104    104       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    107    107       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    138    198
FT   CARBOHYD    174    174       N-LINKED (GLCNAC. . .).
FT                                /FTId=CAR_000055.
FT   DISULFID    244    302
FT   MOD_RES     324    324       REMOVED POST-TRANSLATIONALLY.
FT   CONFLICT    276    276       N -> D (IN REF. 3).
FT   CONFLICT    278    278       N -> D (IN REF. 3).
SQ   SEQUENCE   324 AA;  35704 MW;  A338812F3D1F2C93 CRC64;

  Query Match             69.5%;  Score 405;  DB 1;  Length 324;
  Best Local Similarity   69.6%;  Pred. No. 3.4e-34;
  Matches   71;  Conservative   18;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          9 SVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNS 68
              |||:|||||| | |: ||:|||||||:|::||||||:|:|| |||| |:|:||||||||
Db        116 SVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNS 175

Qy         69 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |:| || | ::|||||||||:||:|::   |: |||||||
Db        176 TFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTK 217


RESULT 11
GC1M_MOUSE
ID   GC1M_MOUSE     STANDARD;      PRT;   393 AA.
AC   P01869;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig gamma-1 chain C region, membrane-bound form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=80045036; PubMed=115593;
RA   Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA   Takahashi N., Mano Y.;
RT   "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT   gamma 1 chain gene.";
RL   Cell 18:559-568(1979).
RN   [2]
RP   SEQUENCE OF 323-393 FROM N.A.
RX   MEDLINE=82197626; PubMed=6804950;
RA   Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RT   "mRNA for surface immunoglobulin gamma chains encodes a highly
RT   conserved transmembrane sequence and a 28-residue intracellular
RT   domain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
RN   [3]
RP   SEQUENCE OF 323-366 FROM N.A.
RX   MEDLINE=82115295; PubMed=6799207;
RA   Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA   Eisenberg D., Wall R.;
RT   "Gene segments encoding transmembrane carboxyl termini of
RT   immunoglobulin gamma chains.";
RL   Cell 26:19-27(1981).
RN   [4]
RP   SEQUENCE OF 1-44 FROM N.A.
RX   MEDLINE=82222190; PubMed=6283537;
```

```
RA   Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT   "Nucleotide sequences of gene segments encoding membrane domains of
RT   immunoglobulin gamma chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Membrane-bound;
CC         IsoId=P01869-1; Sequence=Displayed;
CC       Name=Secreted;
CC         IsoId=P01868-1; Sequence=External;
CC         Note=May be the major isoform;
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; V00793; CAA24172.1; -.
DR   EMBL; V00793; CAA24173.1; -.
DR   EMBL; V00793; CAA24174.1; -.
DR   PIR; B02159; G1MSM.
DR   PDB; 15C8; 23-MAR-99.
DR   PDB; 1AE6; 18-MAR-98.
DR   PDB; 1CL7; 12-JAN-00.
DR   PDB; 1F11; 06-FEB-01.
DR   PDB; 1F58; 29-DEC-99.
DR   PDB; 1KC5; 24-JUL-02.
DR   PDB; 1KCR; 11-MAY-02.
DR   PDB; 25C8; 09-JUL-99.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Alternative splicing; Transmembrane; 3D-structure.
FT   NON_TER       1      1
FT   DOMAIN        1     97       CH1.
FT   DOMAIN       98    110       HINGE.
FT   DOMAIN      111    217       CH2.
FT   DOMAIN      218    324       CH3.
FT   DISULFID     27     82
FT   DISULFID    102    102       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID    104    104       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    107    107       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    138    198
FT   CARBOHYD    174    174       N-LINKED (GLCNAC. . .).
FT   DISULFID    244    302
FT   TRANSMEM    340    357       POTENTIAL.
FT   DOMAIN      358    393       CYTOPLASMIC (POTENTIAL).
SQ   SEQUENCE   393 AA;  43386 MW;  4CC88343B7A1CE27 CRC64;

  Query Match             69.5%;  Score 405;  DB 1;  Length 393;
  Best Local Similarity   69.6%;  Pred. No. 4.3e-34;
  Matches   71;  Conservative   18;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          9 SVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNS 68
              |||:|||||||  | |: ||:|||||||:|::||||||:|:|| |||| |:|:|||||||||
Db        116 SVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNS 175

Qy         69 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |:| || | ::||||||||:||:|::   |: |||||||  |
Db        176 TFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTK 217

RESULT 12
GCC_RAT
ID   GCC_RAT        STANDARD;      PRT;   329 AA.
AC   P20762;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig gamma-2C chain C region.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88166903; PubMed=3127222;
RA   Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
RT   "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
RT   region cDNA: extensive homology to mouse gamma 3.";
RL   Eur. J. Immunol. 18:317-319(1988).
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X07189; CAA30169.1; -.
DR   PIR; S00847; S00847.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region.
FT   NON_TER       1      1
FT   DOMAIN        1     97       CH1.
FT   DOMAIN       98    113       HINGE.
FT   DOMAIN      114    222       CH2.
FT   DOMAIN      223    329       CH3.
FT   DISULFID     15     15       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     82
FT   DISULFID    111    111       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    113    113       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    143    203
FT   DISULFID    249    307
SQ   SEQUENCE   329 AA;  36571 MW;  5FCD7B7933850773 CRC64;

  Query Match             69.1%;  Score 403;  DB 1;  Length 329;
  Best Local Similarity   68.6%;  Pred. No. 5.6e-34;
  Matches   72;  Conservative   17;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          6 GGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQ 65
              | ||||:|||||||  |||: ||:|||||||||:|:|:|:|||:|:|| | |  |:|:| |||
Db        118 GRPSVFIFPPKPKDILMITLTPKVTCVVVDVSEEEPDVQFSWFVDNVRVFTAQTQPHEEQ 177

Qy         66 FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              | |:||| | : ||||::|||:||||:|| ||| |||||||  :
Db        178 LNGTFRVVSTLHIQHQDWMSGKEFKCKVNNKDLPSPIEKTISKPR 222


RESULT 13
GCB_MOUSE
ID   GCB_MOUSE      STANDARD;      PRT;   336 AA.
AC   P01866;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ig gamma-2B chain C region secreted form.
OS   Mus musculus (Mouse).
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ALLELE A).
RX   MEDLINE=80120716; PubMed=6766534;
RA   Yamawaki-Kataoka Y., Kataoka T., Takahashi N., Obata M., Honjo T.;
RT   "Complete nucleotide sequence of immunoglobulin gamma2b chain gene
RT   cloned from newborn nouse DNA.";
RL   Nature 283:786-789(1980).
RN   [2]
RP   SEQUENCE FROM N.A. (MPC 11).
RX   MEDLINE=80081501; PubMed=117548;
RA   Tucker P.W., Marcu K.B., Slightom J.L., Blattner F.R.;
RT   "Structure of the constant and 3' untranslated regions of the murine
RT   gamma 2b heavy chain messenger RNA.";
RL   Science 206:1299-1303(1979).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=80081502; PubMed=117549;
RA   Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R.;
RT   "Sequence of the cloned gene for the constant region of murine gamma
RT   2b immunoglobulin heavy chain.";
RL   Science 206:1303-1306(1979).
RN   [4]
RP   SEQUENCE FROM N.A. (ALLELE B).
RX   MEDLINE=82173203; PubMed=6803173;
RA   Ollo R., Rougeon F.;
RT   "Mouse immunoglobulin allotypes: post-duplication divergence of gamma
RT   2a and gamma 2b chain genes.";
RL   Nature 296:761-763(1982).
RN   [5]
RP   CARBOHYDRATE-LINKAGE SITE THR-105.
RX   MEDLINE=94216359; PubMed=7512967;
RA   Kim H., Yamaguchi Y., Masuda K., Matsunaga C., Yamamoto K.,
RA   Irimura T., Takahashi N., Kato K., Arata Y.;
RT   "O-glycosylation in hinge region of mouse immunoglobulin G2b.";
RL   J. Biol. Chem. 269:12345-12350(1994).
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Secreted;
CC         IsoId=P01866-1; Sequence=Displayed;
CC         Note=May be the major isoform;
CC       Name=Membrane-bound;
CC         IsoId=P01867-1; Sequence=External;
CC   -!- PTM: O-LINKED GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH IS
CC       MODIFIED WITH 2 SIALIC ACID RESIDUES.
CC   -!- PTM: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA CHAINS.
CC   -!- MISCELLANEOUS: The a allele sequence is shown.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
DR   PIR; S25057; G2MS11.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Alternative splicing; Repeat.
FT   NON_TER       1      1
FT   DOMAIN        6     98       IG-LIKE 1.
FT   DOMAIN      127    226       IG-LIKE 2.
FT   DOMAIN      235    331       IG-LIKE 3.
FT   DISULFID     15     15       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     82
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    112    112       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    115    115       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    118    118       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    150    210
FT   DISULFID    256    314
FT   CARBOHYD    105    105       O-LINKED (GALNAC. . .).
FT   MOD_RES     336    336       REMOVED POST-TRANSLATIONALLY (PROBABLE).
FT   VARIANT     163    163       Q -> R (IN ALLELE B).
FT   VARIANT     194    194       T -> A (IN ALLELE B).
FT   VARIANT     300    300       N -> D (IN ALLELE B).
FT   VARIANT     301    301       M -> I (IN ALLELE B).
FT   CONFLICT     25     25       L -> S (IN REF. 2 AND 3).
FT   CONFLICT     36     36       S -> P (IN REF. 2 AND 3).
FT   CONFLICT    239    239       I -> T (IN REF. 2 AND 3).
SQ   SEQUENCE   336 AA;  36658 MW;  7D879662607C356E CRC64;

  Query Match             68.4%;  Score 399;  DB 1;  Length 336;
  Best Local Similarity   65.5%;  Pred. No. 1.5e-33;
  Matches   72;  Conservative   18;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              || : |||||:|||   || |||| ||:|||||||||::||:|| :|:|: |||| |:|:
Db        120 APNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQ 179

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                 | :||| |||| | : ||||::|||:||||:|| ||| ||:|||| |
Db        180 THREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIK 229


RESULT 14
GCBM_MOUSE
ID   GCBM_MOUSE     STANDARD;      PRT;   405 AA.
AC   P01867;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ig gamma-2B chain C region, membrane-bound form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE OF 335-405 FROM N.A.
RX   MEDLINE=82222190; PubMed=6283537;
RA   Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT   "Nucleotide sequences of gene segments encoding membrane domains of
RT   immunoglobulin gamma chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
RN   [2]
RP   SEQUENCE OF 335-378 FROM N.A.
RX   MEDLINE=82115295; PubMed=6799207;
RA   Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA   Eisenberg D., Wall R.;
RT   "Gene segments encoding transmembrane carboxyl termini of
RT   immunoglobulin gamma chains.";
RL   Cell 26:19-27(1981).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Membrane-bound;
CC         IsoId=P01867-1; Sequence=Displayed;
CC       Name=Secreted;
CC         IsoId=P01866-1; Sequence=External;
CC         Note=May be the major isoform;
CC   -!- PTM: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA CHAINS.
CC   -!- MISCELLANEOUS: The sequence of residues 1-335 is assumed to be
CC       identical with the corresponding region of the secreted form.
CC   -!- MISCELLANEOUS: The a allele sequence is shown.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
```

```
DR   EMBL; J00462; AAB59659.1; ALT_INIT.
DR   PIR; C02154; G2MSBM.
DR   PDB; 1CIC; 11-MAR-03.
DR   MGD; MGI:96445; Igh-3.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Transmembrane;
KW   Alternative splicing; 3D-structure; Repeat.
FT   NON_TER       1      1
FT   DOMAIN        6     98       IG-LIKE 1.
FT   DOMAIN      127    226       IG-LIKE 2.
FT   DOMAIN      235    331       IG-LIKE 3.
FT   DISULFID     15     15       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     82
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    112    112       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    115    115       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    118    118       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    150    210
FT   DISULFID    256    314
FT   TRANSMEM    352    369       POTENTIAL.
FT   DOMAIN      370    405       CYTOPLASMIC (POTENTIAL).
SQ   SEQUENCE   405 AA;  44330 MW;  89B3CF0A9B6D49FA CRC64;

  Query Match             68.4%;  Score 399;  DB 1;  Length 405;
  Best Local Similarity   65.5%;  Pred. No. 1.8e-33;
  Matches   72;  Conservative   18;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              || : |||||:|||  || |||| ||:||||||||::||:|| :|:|: |||| |:|:
Db        120 APNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQ 179

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                | :||| |||| | : ||||::|||:|||:|| ||| ||:|||| |
Db        180 THREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIK 229


RESULT 15
GCAB_MOUSE
ID   GCAB_MOUSE     STANDARD;      PRT;   335 AA.
AC   P01864;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ig gamma-2A chain C region secreted form (B allele).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=82037861; PubMed=6170065;
RA   Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT   "Multiple differences between the nucleic acid sequences of the
RT   IgG2aa and IgG2ab alleles of the mouse.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN   [2]
RP   SEQUENCE.
RX   MEDLINE=82037777; PubMed=6794027;
RA   Dognin M.J., Lauwereys M., Strosberg A.D.;
RT   "Multiple amino acid substitutions between murine gamma 2a heavy
RT   chain Fc regions of Ig1a and Ig1b allotypic forms.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Secreted;
CC         IsoId=P01864-1; Sequence=Displayed;
CC         Note=Probably the major isoform;
CC       Name=Membrane-bound;
CC         IsoId=P01865-1; Sequence=External;
CC   -!- MISCELLANEOUS: The sequence differs from that of the a allele,
CC       from BALB/c mice, at 15% of the positions.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00479; -; NOT_ANNOTATED_CDS.
DR   PIR; A02153; G2MSAB.
DR   PDB; 1BOG; 23-MAR-99.
DR   PDB; 1HH6; 26-JAN-01.
DR   PDB; 1HH9; 24-JUL-03.
DR   PDB; 1HI6; 08-FEB-01.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Alternative splicing;
KW   3D-structure; Repeat.
FT   NON_TER       1      1
FT   DOMAIN        6     98       IG-LIKE 1.
FT   DOMAIN      126    225       IG-LIKE 2.
FT   DOMAIN      234    330       IG-LIKE 3.
SQ   SEQUENCE   335 AA;  36596 MW;  FA3382792CBB13C6 CRC64;

  Query Match             67.9%;  Score 396;  DB 1;  Length 335;
  Best Local Similarity   64.5%;  Pred. No. 3e-33;
  Matches   71;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              || : |||||:|||| || |||| :| ||||||||||::||:|| :|:|: |||| |:|:
Db        119 APDLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQ 178

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                | :||| |||| | : ||||::|||:||||:|: ||| |||||||  :
Db        179 THREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNRALPSPIEKTISKPR 228


Search completed: April 29, 2004, 08:44:54
Job time : 11 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 29, 2004, 08:41:02 ; Search time 36 Seconds
(without alignments)
964.083 Million cell updates/sec

Title: US-09-674-857-12
Perfect score: 583
Sequence: 1 APPVAGGPSVFLFPPKPKDT.....CKVSNKGLPSSIEKTISKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	565	96.9	473	4	Q8TC63	Q8tc63 homo sapien
2	541	92.8	469	4	Q7Z7P5	Q7z7p5 homo sapien
3	541	92.8	470	4	Q7Z5W1	Q7z5w1 homo sapien
4	541	92.8	482	4	Q7Z351	Q7z351 homo sapien
5	541	92.8	679	4	Q96PQ8	Q96pq8 homo sapien
6	534	91.6	509	4	Q8NF17	Q8nf17 homo sapien
7	534	91.6	521	4	Q8N4Y9	Q8n4y9 homo sapien
8	531	91.1	354	4	Q86TT2	Q86tt2 homo sapien
9	462	79.2	337	6	Q95M34	Q95m34 equus cabal
10	417	71.5	470	11	Q7TMK1	Q7tmk1 mus musculu
11	409	70.2	469	11	Q8R3V9	Q8r3v9 mus musculu
12	405	69.5	437	11	Q9R1A4	Q9r1a4 mus musculu
13	405	69.5	463	11	Q99LC4	Q99lc4 mus musculu
14	399	68.4	473	11	Q91Z05	Q91z05 mus musculu
15	399	68.4	474	11	Q8R3H6	Q8r3h6 mus musculu
16	396	67.9	473	11	Q9D8L4	Q9d814 mus musculu
17	384	65.9	468	11	Q99L31	Q99131 mus musculu
18	384	65.9	473	11	Q99L25	Q99125 mus musculu
19	138	23.7	375	4	Q86TT1	Q86tt1 homo sapien
20	138	23.7	588	4	Q8WUX4	Q8wux4 homo sapien
21	138	23.7	597	4	Q9BU10	Q9bu10 homo sapien
22	138	23.7	597	4	Q9BQB8	Q9bqb8 homo sapien
23	138	23.7	597	4	Q96BB9	Q96bb9 homo sapien
24	138	23.7	613	4	Q96EY0	Q96ey0 homo sapien
25	138	23.7	613	4	Q8WUK1	Q8wuk1 homo sapien
26	138	23.7	614	4	Q96GA6	Q96ga6 homo sapien
27	138	23.7	618	4	Q96AA6	Q96aa6 homo sapien
28	133	22.8	234	4	Q7Z473	Q7z473 homo sapien
29	133	22.8	236	4	Q7Z3Y4	Q7z3y4 homo sapien
30	133	22.8	239	4	Q8NEK0	Q8nek0 homo sapien
31	133	22.8	239	4	Q8TCD0	Q8tcd0 homo sapien
32	132	22.6	613	11	Q8VCX7	Q8vcx7 mus musculu
33	132	22.6	614	11	Q7TMT6	Q7tmt6 mus musculu
34	124.5	21.4	478	4	Q7Z379	Q7z379 homo sapien
35	121	20.8	497	4	Q8WY24	Q8wy24 homo sapien
36	120.5	20.7	130	11	Q9D8W4	Q9d8w4 mus musculu
37	120.5	20.7	384	4	Q9UP60	Q9up60 homo sapien
38	120.5	20.7	416	4	Q9NPP6	Q9npp6 homo sapien
39	120.5	20.7	492	4	Q7Z374	Q7z374 homo sapien
40	120.5	20.7	493	4	Q8NCL6	Q8ncl6 homo sapien
41	120.5	20.7	494	4	Q96K68	Q96k68 homo sapien
42	120.5	20.7	496	4	Q96DK0	Q96dk0 homo sapien
43	120.5	20.7	496	4	Q96KX8	Q96kx8 homo sapien
44	120.5	20.7	499	4	Q8N5K4	Q8n5k4 homo sapien
45	118.5	20.3	684	13	Q90544	Q90544 ginglymosto

ALIGNMENTS

RESULT 1
Q8TC63
ID Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC025985; AAH25985.1; -.
DR GO; GO:0005507; F:copper ion binding; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 96.9%; Score 565; DB 4; Length 473;
Best Local Similarity 97.3%; Pred. No. 2e-55;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60

```
Db        257 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 316

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 366


RESULT 2
Q7Z7P5
ID   Q7Z7P5      PRELIMINARY;      PRT;   469 AA.
AC   Q7Z7P5;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC051328; AAH51328.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   469 AA;  51395 MW;  C8D5BE12BAAF795C CRC64;

  Query Match             92.8%;  Score 541;  DB 4;  Length 469;
  Best Local Similarity   91.8%;  Pred. No. 1e-52;
  Matches  101;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||| |||||:||||||||||||||||||
Db        253 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 312

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||:|||||||||||||||||||||||||||| ||: |||||||||
Db        313 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 362


RESULT 3
Q7Z5W1
ID   Q7Z5W1      PRELIMINARY;      PRT;   470 AA.
AC   Q7Z5W1;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC053984; AAH53984.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51204 MW;  778CF34521483E1A CRC64;

  Query Match             92.8%;  Score 541;  DB 4;  Length 470;
  Best Local Similarity   91.8%;  Pred. No. 1e-52;
  Matches  101;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||| |||||:||||||||||||||||||
Db        254 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 313

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||:|||||||||||||||||||||||||||| ||: |||||||||
Db        314 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 363


RESULT 4
Q7Z351
ID   Q7Z351      PRELIMINARY;      PRT;   482 AA.
AC   Q7Z351;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein DKFZp686N02209.
GN   DKFZP686N02209.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human rectum tumor;
RA   Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX538118; CAD98026.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   482 AA;  52852 MW;  EDA75F1901D1A034 CRC64;
```

```
  Query Match             92.8%;  Score 541;  DB 4;  Length 482;
  Best Local Similarity   91.8%;  Pred. No. 1.1e-52;
  Matches  101;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||| |||||:||||||||||||||||
Db        266 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 325

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||:|||||||||||||||||||||||||||| ||: |||||||||
Db        326 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 375


RESULT 5
Q96PQ8
ID   Q96PQ8      PRELIMINARY;      PRT;   679 AA.
AC   Q96PQ8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Factor VII active site mutant immunoconjugate.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21477448; PubMed=11593034;
RA   Hu Z., Garen A.;
RT   "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT   cells for immunotherapy in mouse models of prostatic cancer.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Hu Z., Garen A.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF272774; AAK58686.2; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR000152; Asx_hydroxyl_S.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR001881; EGF_Ca.
DR   InterPro; IPR001438; EGF_II.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002383; GLA_blood.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR000294; VitK_dep_GLA.
DR   Pfam; PF00008; EGF; 2.
DR   Pfam; PF00594; gla; 1.
DR   Pfam; PF00047; ig; 2.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00010; EGFBLOOD.
DR   PRINTS; PR00001; GLABLOOD.
DR   SMART; SM00181; EGF; 2.
DR   SMART; SM00179; EGF_CA; 1.
DR   SMART; SM00069; GLA; 1.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00010; ASX_HYDROXYL; 1.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01187; EGF_CA; 1.
DR   PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
SQ   SEQUENCE   679 AA;  75552 MW;  0B0023AE70A067A1 CRC64;

  Query Match             92.8%;  Score 541;  DB 4;  Length 679;
  Best Local Similarity   91.8%;  Pred. No. 1.6e-52;
  Matches  101;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||| |||||:||||||||||||||||
Db        463 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 522

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||:|||||||||||||||||||||||||||| ||: |||||||||
Db        523 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 572


RESULT 6
Q8NF17
ID   Q8NF17      PRELIMINARY;      PRT;   509 AA.
AC   Q8NF17;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   FLJ00385 protein (Fragment).
GN   FLJ00385.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RT   "The nucleotide sequence of a long cDNA clone isolated from human
RT   spleen.";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK090464; BAC03445.1; -.
DR   PIR; A45874; A45874.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 3.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
FT   NON_TER      1      1
SQ   SEQUENCE   509 AA;  56111 MW;  089498D8076E863C CRC64;

  Query Match             91.6%;  Score 534;  DB 4;  Length 509;
  Best Local Similarity   90.9%;  Pred. No. 7.1e-52;
  Matches  100;  Conservative    3;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||| ||||||| ||||||||||||||
Db        224 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 283

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||:|||||||||||||||||||||||||| ||: ||||||| |
Db        284 PREEQFNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 333


RESULT 7
Q8N4Y9
ID   Q8N4Y9      PRELIMINARY;      PRT;   521 AA.
AC   Q8N4Y9;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
```

```
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC033178; AAH33178.1; -.
DR   PIR; A60764; A60764.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   521 AA;  57156 MW;  2AC7D22E72D6CAA2 CRC64;

  Query Match             91.6%;  Score 534;  DB 4;  Length 521;
  Best Local Similarity   90.9%;  Pred. No. 7.3e-52;
  Matches  100;  Conservative    3;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||| |||||||| ||||||||||||||
Db        305 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 364

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||||||:|||||||||||||||||||||||||||| ||: ||||||| |
Db        365 PREEQFNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 414


RESULT 8
Q86TT2
ID   Q86TT2      PRELIMINARY;      PRT;   354 AA.
AC   Q86TT2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Human full-length cDNA clone CS0DI019YF20 of placenta of Homo sapiens
DE   (Human) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RA   Genoscope;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RA   Li W.B., Gruber C., Jessee J., Polayes D.;
RT   "Full-length cDNA libraries and normalization.";
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX248278; CAD62606.1; -.
DR   GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00407; IGc1; 3.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Plasmid.
FT   NON_TER       1      1
SQ   SEQUENCE   354 AA;  39125 MW;  23B80BF4D2B87A92 CRC64;

  Query Match             91.1%;  Score 531;  DB 4;  Length 354;
  Best Local Similarity   90.0%;  Pred. No. 9.9e-52;
  Matches   99;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              || : |||||||||||||||||||||||||||||||| |||||||| ||||||||||||||
Db        138 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 197

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |||||:|||:|||||||||||||||||||||||||| ||: ||||||| |
Db        198 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 247


RESULT 9
Q95M34
ID   Q95M34      PRELIMINARY;      PRT;   337 AA.
AC   Q95M34;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Immunogobulin gamma 1 heavy chain constant region (Fragment).
GN   IGHC1.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wagner B.;
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98383416; PubMed=9717671;
RA   Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA   Leibold W., Radbruch A.;
RT   "Organization of the equine immunoglobulin heavy chain constant region
RT   genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL   Immunobiology 199:105-119(1998).
DR   EMBL; AJ300575; CAC44624.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
FT   NON_TER       1      1
SQ   SEQUENCE   337 AA;  37438 MW;  A60BF2B01DEFD1F6 CRC64;

  Query Match             79.2%;  Score 462;  DB 6;  Length 337;
  Best Local Similarity   74.5%;  Pred. No. 6.3e-44;
  Matches   82;  Conservative   16;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              || : ||||||:||| |||||||:||||||||||||||:|:|:||||:|||||  | |:
Db        119 APELLGGPSVFIFPPNPKDTLMITRTPEVTCVVVDVSQENPDVKFNWYMDGVEVRTATTR 178

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |:|||||||||||| : |||||:|||:||||:|: ||  ||:||:| |
Db        179 PKEEQFNSTYRVVSVLRIQHQDWLSGKEFKCKVNNQALPQPIERTITKTK 228


RESULT 10
Q7TMK1
ID   Q7TMK1      PRELIMINARY;      PRT;   470 AA.
AC   Q7TMK1;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Breast tumor;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Breast tumor;
RA   Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC055910; AAH55910.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51727 MW;  6D90E4DF896BB090 CRC64;

  Query Match             71.5%;  Score 417;  DB 11;  Length 470;
  Best Local Similarity   67.6%;  Pred. No. 1.2e-38;
  Matches   75;  Conservative   17;  Mismatches   17;  Indels    2;  Gaps    1;

Qy          2 PP--VAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKT 59
              ||  : |||||||:|||||||| |||| ||:|||||||||::||:|  :|:||  ||| | |
Db        253 PPGNILGGPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWT 312

Qy         60 KPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              :||| |:|||:|||| | : |||| ||||:||||:|| ||: ||:|||| |
Db        313 QPREAQYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPK 363


RESULT 11
Q8R3V9
ID   Q8R3V9      PRELIMINARY;      PRT;   469 AA.
AC   Q8R3V9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   IGH-4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC024405; AAH24405.1; -.
DR   PIR; B45837; B45837.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   469 AA;  51976 MW;  534793F155D05457 CRC64;

  Query Match             70.2%;  Score 409;  DB 11;  Length 469;
  Best Local Similarity   70.6%;  Pred. No. 9.7e-38;
  Matches   72;  Conservative   17;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          9 SVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNS 68
              |||:||||||| | |: ||:|||||||:|::||||||:|:|| |||| |:|||||||||
Db        261 SVFIPPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTKPREEQFNS 320

Qy         69 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |:| || | ::|||||||||:||:|::   |: |||||||
Db        321 TFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTK 362


RESULT 12
Q9R1A4
ID   Q9R1A4      PRELIMINARY;      PRT;   437 AA.
AC   Q9R1A4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Gamma1 heavy chain of Mab7 (Fragment).
GN   IGH-4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT   "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT   antibody (Mab 7, its light and heavy chains) and construction of a
RT   single chain antibody (scFV).";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF152372; AAD40243.1; -.
DR   PIR; B45837; B45837.
DR   PDB; 1CQK; 11-SEP-99.
DR   PDB; 1I9I; 25-DEC-02.
DR   PDB; 1KCU; 11-MAY-02.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
FT   NON_TER       1      1
FT   NON_TER     437    437
SQ   SEQUENCE   437 AA;  48142 MW;  5C3A7BB3EE7D697C CRC64;

  Query Match             69.5%;  Score 405;  DB 11;  Length 437;
  Best Local Similarity   69.6%;  Pred. No. 2.5e-37;
  Matches   71;  Conservative   18;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          9 SVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNS 68
              |||:||||||| | |: ||:||||||||:|::||||||:|:|| |||| |:|:||||||||
Db        229 SVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNS 288

Qy         69 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |:| || | ::|||||||||:||:|::   |: |||||||
Db        289 TFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTK 330


RESULT 13
Q99LC4
ID   Q99LC4      PRELIMINARY;      PRT;   463 AA.
AC   Q99LC4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
```

```
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to RIKEN cDNA 1810060O09 gene.
GN   IGH-4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003435; AAH03435.1; -.
DR   PIR; B45837; B45837.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
SQ   SEQUENCE   463 AA;  51007 MW;  EAA674C6BBC30783 CRC64;

  Query Match             69.5%;  Score 405;  DB 11;  Length 463;
  Best Local Similarity   69.6%;  Pred. No. 2.7e-37;
  Matches   71;  Conservative   18;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          9 SVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNS 68
              |||:|||||||| | |: ||:|||||||:|::|||||||:|:|| |||| |:|:|||||||
Db        255 SVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNS 314

Qy         69 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              |:| || | ::|||||||||:||:|::   |: ||||||| |
Db        315 TFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTK 356


RESULT 14
Q91Z05
ID   Q91Z05      PRELIMINARY;      PRT;   473 AA.
AC   Q91Z05;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   AU044919.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC010327; AAH10327.1; -.
DR   MGD; MGI:2144967; AU044919.
DR   GO; GO:0005489; F:electron transporter activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR000345; CytC_heme_BS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00190; CYTOCHROME_C; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;  51946 MW;  CF625F008932AF12 CRC64;

  Query Match             68.4%;  Score 399;  DB 11;  Length 473;
  Best Local Similarity   65.5%;  Pred. No. 1.3e-36;
  Matches   72;  Conservative   18;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              || : |||||||:|||  || |||| ||:||||||||||::||:|| :|:|: |||| |:|:
Db        257 APNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQ 316

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                | :||| |||| | : ||||::|||:||||:|| ||| ||:|||| |
Db        317 THREDYNSTIRVVSALPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIK 366


RESULT 15
Q8R3H6
ID   Q8R3H6      PRELIMINARY;      PRT;   474 AA.
AC   Q8R3H6;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   AU044919.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC025447; AAH25447.1; -.
DR   MGD; MGI:2144967; AU044919.
DR   GO; GO:0005489; F:electron transporter activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR000345; CytC_heme_BS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00190; CYTOCHROME_C; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   474 AA;  51748 MW;  8608B57C6CD2874A CRC64;

  Query Match             68.4%;  Score 399;  DB 11;  Length 474;
  Best Local Similarity   65.5%;  Pred. No. 1.3e-36;
  Matches   72;  Conservative   18;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              || : |||||||:|||  || |||| ||:||||||||||::||:|| :|:|: |||| |:|:
Db        258 APNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQ 317

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                | :||| |||| | : ||||::|||:||||:|| ||| ||:|||| |
Db        318 THREDYNSTIRVVSALPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIK 367


Search completed: April 29, 2004, 08:46:18
Job time : 36 secs
```

OM protein - protein search, using sw model

Run on: April 29, 2004, 08:46:23 ; Search time 38.5 Seconds
(without alignments)
791.970 Million cell updates/sec

Title: US-09-674-857-12
Perfect score: 583
Sequence: 1 APPVAGGPSVFLFPPKPKDT.....CKVSNKGLPSSIEKTISKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 277189581 residues

Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	570	97.8	437	10	US-09-932-812-20	Sequence 20, Appl
2	570	97.8	449	10	US-09-968-362-20	Sequence 20, Appl
3	566.5	97.2	472	14	US-10-006-593-67	Sequence 67, Appl
4	566.5	97.2	472	15	US-10-307-724-67	Sequence 67, Appl
5	565	96.9	218	12	US-09-813-341-5	Sequence 5, Appli
6	565	96.9	218	14	US-10-277-307-5	Sequence 5, Appli
7	565	96.9	218	14	US-10-277-370-5	Sequence 5, Appli
8	565	96.9	218	14	US-10-196-394-76	Sequence 76, Appl
9	565	96.9	218	15	US-10-370-749-18	Sequence 18, Appl
10	565	96.9	284	12	US-10-433-108-24	Sequence 24, Appl
11	565	96.9	327	9	US-09-925-664-47	Sequence 47, Appl
12	565	96.9	327	13	US-10-047-542-26	Sequence 26, Appl
13	565	96.9	327	14	US-10-310-719-7	Sequence 7, Appli
14	565	96.9	327	14	US-10-112-582-4	Sequence 4, Appli
15	565	96.9	329	9	US-09-935-868-12	Sequence 12, Appl
16	565	96.9	329	10	US-09-990-586-100	Sequence 100, App
17	565	96.9	329	14	US-10-287-035-12	Sequence 12, Appl
18	565	96.9	329	14	US-10-282-162-12	Sequence 12, Appl
19	565	96.9	329	14	US-10-310-113-169	Sequence 169, App
20	565	96.9	329	14	US-10-230-880-100	Sequence 100, App
21	565	96.9	382	12	US-10-050-227-7	Sequence 7, Appli
22	565	96.9	382	12	US-10-050-227-10	Sequence 10, Appl
23	565	96.9	396	9	US-09-859-361-2	Sequence 2, Appli
24	565	96.9	396	9	US-09-859-361-5	Sequence 5, Appli
25	565	96.9	417	14	US-10-005-438-2	Sequence 2, Appli
26	565	96.9	443	9	US-09-917-410-4	Sequence 4, Appli
27	565	96.9	444	10	US-09-256-156-4	Sequence 4, Appli
28	565	96.9	448	9	US-09-917-410-6	Sequence 6, Appli
29	565	96.9	465	14	US-10-401-344-2	Sequence 2, Appli
30	565	96.9	467	14	US-10-211-357-8	Sequence 8, Appli
31	565	96.9	467	14	US-10-211-357-10	Sequence 10, Appl
32	565	96.9	467	14	US-10-211-357-12	Sequence 12, Appl
33	565	96.9	467	15	US-10-428-408A-30	Sequence 30, Appl
34	565	96.9	778	9	US-09-935-868-46	Sequence 46, Appl
35	565	96.9	778	9	US-09-935-868-50	Sequence 50, Appl
36	565	96.9	778	14	US-10-287-035-46	Sequence 46, Appl
37	565	96.9	778	14	US-10-287-035-50	Sequence 50, Appl
38	565	96.9	778	14	US-10-287-035-56	Sequence 56, Appl
39	565	96.9	778	14	US-10-287-035-60	Sequence 60, Appl
40	565	96.9	782	9	US-09-935-868-48	Sequence 48, Appl
41	565	96.9	782	9	US-09-935-868-52	Sequence 52, Appl
42	565	96.9	782	14	US-10-287-035-48	Sequence 48, Appl
43	565	96.9	782	14	US-10-287-035-52	Sequence 52, Appl
44	565	96.9	782	14	US-10-287-035-54	Sequence 54, Appl
45	565	96.9	782	14	US-10-287-035-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-09-932-812-20
; Sequence 20, Application US/09932812
; Publication No. US20030082749A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biolog
; FILE REFERENCE: 02SUN2001
; CURRENT APPLICATION NUMBER: US/09/932,812
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HuEPO-L-vFc gamma4 with a 27-amino acid leader peptide (Figure 2
; OTHER INFORMATION:)
US-09-932-812-20

Query Match 97.8%; Score 570; DB 10; Length 437;
Best Local Similarity 98.2%; Pred. No. 4.8e-50;
Matches 108; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 APEPAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 280

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 330
```

RESULT 2
US-09-968-362-20

```
; Sequence 20, Application US/09968362
; Publication No. US20030082679A1
; GENERAL INFORMATION:
;  APPLICANT: Sun, Lee-Hwei K
;  APPLICANT: Sun, Bill
;  APPLICANT: Sun, Cecily R
;  TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulaing factor
;  TITLE OF INVENTION: biological activities
;  FILE REFERENCE: 03SUN2001
;  CURRENT APPLICATION NUMBER: US/09/968,362
;  CURRENT FILING DATE: 2001-10-30
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 449
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: hG-CSF-L-vFc gamma4 with a 30-amino acid leader peptide (Figure 2
;   OTHER INFORMATION: B)
US-09-968-362-20

  Query Match             97.8%;  Score 570;  DB 10;  Length 449;
  Best Local Similarity   98.2%;  Pred. No. 4.9e-50;
  Matches  108;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 APEFAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 292

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 342


RESULT 3
US-10-006-593-67
; Sequence 67, Application US/10006593
; Publication No. US20030049683A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Frederickson, Shana
;  APPLICANT:  Renshaw, Mark
;  TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
;  FILE REFERENCE: 1087-2
;  CURRENT APPLICATION NUMBER: US/10/006,593
;  CURRENT FILING DATE:  2001-12-05
;  PRIOR APPLICATION NUMBER: US 60/251,448
;  PRIOR FILING DATE: 2000-12-05
;  PRIOR APPLICATION NUMBER: US 60/288,889
;  PRIOR FILING DATE: 2001-05-04
;  PRIOR APPLICATION NUMBER: US 60/294,068
;  PRIOR FILING DATE: 2001-05-29
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
;   LENGTH: 472
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Humanized antibody heavy chain
US-10-006-593-67

  Query Match             97.2%;  Score 566.5;  DB 14;  Length 472;
  Best Local Similarity   99.1%;  Pred. No. 1.2e-49;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              |||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 315

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 365


RESULT 4
US-10-307-724-67
; Sequence 67, Application US/10307724
; Publication No. US20030232972A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Frederickson, Shana
;  APPLICANT:  Renshaw, Mark
;  TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
;  FILE REFERENCE: 1087-2cip
;  CURRENT APPLICATION NUMBER: US/10/307,724
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: US 60/251,448
;  PRIOR FILING DATE: 2000-12-05
;  PRIOR APPLICATION NUMBER: US 60/288,889
;  PRIOR FILING DATE: 2001-05-04
;  PRIOR APPLICATION NUMBER: US 60/294,068
;  PRIOR FILING DATE: 2001-05-29
;  PRIOR APPLICATION NUMBER: US 10/006,593
;  PRIOR FILING DATE: 2001-12-05
;  NUMBER OF SEQ ID NOS: 134
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
;   LENGTH: 472
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Humanized antibody heavy chain
US-10-307-724-67

  Query Match             97.2%;  Score 566.5;  DB 15;  Length 472;
  Best Local Similarity   99.1%;  Pred. No. 1.2e-49;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              |||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 315

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 365


RESULT 5
US-09-813-341-5
; Sequence 5, Application US/09813341
; Publication No. US20020004587A1
; GENERAL INFORMATION:
;  APPLICANT: Miller, Kathy L.
;  APPLICANT:  Presta, Leonard G.
;  TITLE OF INVENTION: MULTIVALENT ANTIBODIES AND USES THEREFOR
;  FILE REFERENCE: P1780R1
;  CURRENT APPLICATION NUMBER: US/09/813,341
;  CURRENT FILING DATE:  2001-03-20
;  PRIOR APPLICATION NUMBER: US 60/195,819
;  PRIOR FILING DATE: 2000-04-11
;  NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
;   LENGTH: 218
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-813-341-5

  Query Match             96.9%;  Score 565;  DB 12;  Length 218;
  Best Local Similarity   97.3%;  Pred. No. 6.8e-50;
  Matches  107;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 61
```

```
Qy          61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 111
```

RESULT 6
US-10-277-307-5
; Sequence 5, Application US/10277307
; Publication No. US20030139908A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Glycoprotein Compositions
; FILE REFERENCE: P1877R1
; CURRENT APPLICATION NUMBER: US/10/277,307
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: US 60/337,642
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/347,694
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 5
; LENGTH: 218
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-277-307-5

```
  Query Match             96.9%;  Score 565;  DB 14;  Length 218;
  Best Local Similarity   97.3%;  Pred. No. 6.8e-50;
  Matches  107;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy           1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
               ||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           2 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 61

Qy          61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 111
```

RESULT 7
US-10-277-370-5
; Sequence 5, Application US/10277370
; Publication No. US20030157108A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Glycoprotein Compositions
; FILE REFERENCE: P1877R1
; CURRENT APPLICATION NUMBER: US/10/277,370
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US 60/337,642
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/347,694
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 5
; LENGTH: 218
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-277-370-5

```
  Query Match             96.9%;  Score 565;  DB 14;  Length 218;
  Best Local Similarity   97.3%;  Pred. No. 6.8e-50;
  Matches  107;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy           1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
               ||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           2 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 61

Qy          61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 111
```

RESULT 8
US-10-196-394-76
; Sequence 76, Application US/10196394
; Publication No. US20030171278A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: Compounds that Bind HER2
; FILE REFERENCE: P1713R1
; CURRENT APPLICATION NUMBER: US/10/196,394
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US/09/609,721
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/142,232
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 76
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-196-394-76

```
  Query Match             96.9%;  Score 565;  DB 14;  Length 218;
  Best Local Similarity   97.3%;  Pred. No. 6.8e-50;
  Matches  107;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy           1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
               ||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           2 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 61

Qy          61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 111
```

RESULT 9
US-10-370-749-18
; Sequence 18, Application US/10370749
; Publication No. US20040002587A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffry D.
; APPLICANT: Allan, Barrett
; TITLE OF INVENTION: Fc Region Variants
; FILE REFERENCE: AME-07823
; CURRENT APPLICATION NUMBER: US/10/370,749
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/358,161
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-370-749-18

```
  Query Match             96.9%;  Score 565;  DB 15;  Length 218;
  Best Local Similarity   97.3%;  Pred. No. 6.8e-50;
  Matches  107;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy           1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
               ||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           2 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 61

Qy          61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 111
```

RESULT 10
US-10-433-108-24
; Sequence 24, Application US/10433108
; Publication No. US20040053370A1

; GENERAL INFORMATION:
; APPLICANT: Eli Lilly and Company
; TITLE OF INVENTION: GLP-1 FUSION PROTEINS
; FILE REFERENCE: X-13991
; CURRENT APPLICATION NUMBER: US/10/433,108
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: US 60/251,954
; PRIOR FILING DATE: 2000-06-12
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-433-108-24

Query Match 96.9%; Score 565; DB 12; Length 284;
Best Local Similarity 97.3%; Pred. No. 9.3e-50;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 68 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 127

Qy 61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
Db 128 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 177

RESULT 11
US-09-925-664-47
; Sequence 47, Application US/09925664
; Patent No. US20020160006A1
; GENERAL INFORMATION:
; APPLICANT: Denney, Jr., Dan W.
; TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
; FILE REFERENCE: GENITOPE-06499
; CURRENT APPLICATION NUMBER: US/09/925,664
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/370,453
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: 08/644,664
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/761,277
; PRIOR FILING DATE: 1996-12-06
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-664-47

Query Match 96.9%; Score 565; DB 9; Length 327;
Best Local Similarity 97.3%; Pred. No. 1.1e-49;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 111 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 170

Qy 61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
Db 171 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 220

RESULT 12
US-10-047-542-26
; Sequence 26, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; TITLE OF INVENTION: AND BACTERIAL DISEASES
; FILE REFERENCE: 030905.0004.CIP1
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-047-542-26

Query Match 96.9%; Score 565; DB 13; Length 327;
Best Local Similarity 97.3%; Pred. No. 1.1e-49;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 111 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 170

Qy 61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
Db 171 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 220

RESULT 13
US-10-310-719-7
; Sequence 7, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc
; LOCATION: (1)..(327)
; OTHER INFORMATION: Human gamma 4 constant region
US-10-310-719-7

Query Match 96.9%; Score 565; DB 14; Length 327;
Best Local Similarity 97.3%; Pred. No. 1.1e-49;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 111 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 170

Qy 61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
Db 171 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 220

RESULT 14
US-10-112-582-4

; Sequence 4, Application US/10112582
; Publication No. US20030166877A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
; FILE REFERENCE: LEX-017
; CURRENT APPLICATION NUMBER: US/10/112,582
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/280,625
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Ig gamma-4 chain C region
US-10-112-582-4

Query Match 96.9%; Score 565; DB 14; Length 327;
Best Local Similarity 97.3%; Pred. No. 1.1e-49;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 170

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 220
```

RESULT 15
US-09-935-868-12
; Sequence 12, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-12

Query Match 96.9%; Score 565; DB 9; Length 329;
Best Local Similarity 97.3%; Pred. No. 1.1e-49;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        113 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 172

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        173 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 222
```

Search completed: April 29, 2004, 08:55:55
Job time : 39.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 29, 2004, 08:42:33 ; Search time 16.5 Seconds
(without alignments)
344.173 Million cell updates/sec

Title: US-09-674-857-12
Perfect score: 583
Sequence: 1 APPVAGGPSVFLFPPKPKDT.....CKVSNKGLPSSIEKTISKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	565	96.9	110	3	US-08-444-644-44	Sequence 44, Appl
2	565	96.9	110	4	US-08-232-246A-44	Sequence 44, Appl
3	565	96.9	327	2	US-08-761-277A-47	Sequence 47, Appl
4	565	96.9	329	4	US-09-313-942-12	Sequence 12, Appl
5	565	96.9	382	1	US-08-470-299-7	Sequence 7, Appli
6	565	96.9	382	1	US-08-470-299-10	Sequence 10, Appl
7	565	96.9	443	5	PCT-US96-13152-4	Sequence 4, Appli
8	565	96.9	467	1	US-08-704-744-81	Sequence 81, Appl
9	565	96.9	467	2	US-07-916-098A-45	Sequence 45, Appl
10	565	96.9	467	3	US-08-523-894-8	Sequence 8, Appli
11	565	96.9	467	3	US-08-523-894-10	Sequence 10, Appl
12	565	96.9	467	3	US-08-523-894-12	Sequence 12, Appl
13	561	96.2	109	2	US-08-070-116A-4	Sequence 4, Appli
14	561	96.2	109	4	US-09-557-050-4	Sequence 4, Appli
15	559	95.9	326	3	US-08-808-720-3	Sequence 3, Appli
16	559	95.9	328	3	US-08-808-720-1	Sequence 1, Appli
17	559	95.9	331	3	US-08-808-720-5	Sequence 5, Appli
18	559	95.9	331	3	US-08-808-720-7	Sequence 7, Appli
19	559	95.9	374	4	US-09-227-595-26	Sequence 26, Appl
20	559	95.9	374	4	US-09-227-595-28	Sequence 28, Appl
21	546	93.7	468	4	US-09-485-737B-67	Sequence 67, Appl
22	546	93.7	488	4	US-09-499-846-12	Sequence 12, Appl
23	546	93.7	497	4	US-09-499-846-10	Sequence 10, Appl
24	546	93.7	525	4	US-09-499-846-8	Sequence 8, Appli
25	546	93.7	711	4	US-09-485-737B-90	Sequence 90, Appl
26	542.5	93.1	109	3	US-08-444-644-30	Sequence 30, Appl
27	542.5	93.1	109	4	US-08-232-246A-30	Sequence 30, Appl
28	542.5	93.1	432	3	US-08-477-460B-2	Sequence 2, Appli
29	542.5	93.1	432	3	US-08-379-516-2	Sequence 2, Appli
30	542.5	93.1	432	3	US-09-329-916-2	Sequence 2, Appli
31	542.5	93.1	432	3	US-08-485-372A-2	Sequence 2, Appli
32	542.5	93.1	432	4	US-09-409-006A-2	Sequence 2, Appli
33	542.5	93.1	432	4	US-08-484-681-2	Sequence 2, Appli
34	542.5	93.1	432	5	PCT-US93-07422-2	Sequence 2, Appli
35	542.5	93.1	451	4	US-09-472-087-70	Sequence 70, Appl
36	542.5	93.1	463	4	US-09-472-087-1	Sequence 1, Appli
37	542.5	93.1	463	4	US-09-472-087-4	Sequence 4, Appli
38	542.5	93.1	463	4	US-09-472-087-63	Sequence 63, Appl
39	542.5	93.1	463	4	US-09-472-087-68	Sequence 68, Appl
40	542.5	93.1	464	4	US-09-472-087-2	Sequence 2, Appli
41	542.5	93.1	464	4	US-09-472-087-66	Sequence 66, Appl
42	542.5	93.1	530	3	US-08-477-460B-4	Sequence 4, Appli
43	542.5	93.1	530	3	US-08-379-516-4	Sequence 4, Appli
44	542.5	93.1	530	3	US-09-329-916-4	Sequence 4, Appli
45	542.5	93.1	530	3	US-08-485-372A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-444-644-44
; Sequence 44, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

```
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-444-644-44

  Query Match             96.9%;  Score 565;  DB 3;  Length 110;
  Best Local Similarity   97.3%;  Pred. No. 9.6e-61;
  Matches  107;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110


RESULT 2
US-08-232-246A-44
; Sequence 44, Application US/08232246A
; Patent No. 6329508
;  GENERAL INFORMATION:
;    APPLICANT:  Friden, Phillip M.
;    TITLE OF INVENTION:  TRANSFERRIN RECEPTOR SPECIFIC
;    TITLE OF INVENTION:  ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
;    TITLE OF INVENTION:  CONJUGATES
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,246A
;      FILING DATE:  04-MAY-1994
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/800,458
;      FILING DATE:  26-NOV-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US90/05077
;      FILING DATE:  07-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/404,089
;      FILING DATE:  07-SEP-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wagner, Richard W.
;      REGISTRATION NUMBER:  34,480
;      REFERENCE/DOCKET NUMBER:  ALK88-15AAA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  110 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-232-246A-44

  Query Match             96.9%;  Score 565;  DB 4;  Length 110;
  Best Local Similarity   97.3%;  Pred. No. 9.6e-61;
  Matches  107;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110


RESULT 3
US-08-761-277A-47
; Sequence 47, Application US/08761277A
; Patent No. 5972334
;  GENERAL INFORMATION:
;    APPLICANT:  Denney Jr., Dan W.
;    TITLE OF INVENTION:  Vaccines For Treatment Of Lymphoma And
;    TITLE OF INVENTION:  Leukemia
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/761,277A
;      FILING DATE:  06-DEC-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/644,664
;      FILING DATE:  01-MAY-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MacKnight, Kamrin T.
;      REGISTRATION NUMBER:  38,230
;      REFERENCE/DOCKET NUMBER:  GENITOPE-02406
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  47:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  327 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-761-277A-47

  Query Match             96.9%;  Score 565;  DB 2;  Length 327;
  Best Local Similarity   97.3%;  Pred. No. 4.2e-60;
  Matches  107;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 170

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 220


RESULT 4
US-09-313-942-12
; Sequence 12, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
;  APPLICANT: REGENERON PHARMACEUTICALS, INC.
;  TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
;  TITLE OF INVENTION:  AND USING
;  FILE REFERENCE: REG 203-A
```

```
;  CURRENT APPLICATION NUMBER: US/09/313,942
;  CURRENT FILING DATE:  1999-05-19
;  PRIOR APPLICATION NUMBER: 09/313,942
;  PRIOR FILING DATE: 1999-05-19
;  PRIOR APPLICATION NUMBER: 60/101,858
;  PRIOR FILING DATE: 1998-09-25
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
;   LENGTH: 329
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-313-942-12

  Query Match             96.9%;  Score 565;  DB 4;  Length 329;
  Best Local Similarity   97.3%;  Pred. No. 4.3e-60;
  Matches  107;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        113 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 172

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        173 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 222


RESULT 5
US-08-470-299-7
; Sequence 7, Application US/08470299
; Patent No. 5783181
;  GENERAL INFORMATION:
;    APPLICANT:  Browne, Michael J.
;    APPLICANT:  Murphy, Kay E.
;    APPLICANT:  Chapman, Conrad G.
;    APPLICANT:  Clinkenbeard, Helen E.
;    APPLICANT:  Young, Peter R.
;    APPLICANT:  Shatzman, Allan R.
;    TITLE OF INVENTION:  No. 5783181el Compounds
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham Corporation
;      STREET:  709 Swedeland Road, P.O. Box 1539
;      CITY:  King of Prussia
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19406
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,299
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sutton, Jeffrey A.
;      REGISTRATION NUMBER:  34,028
;      REFERENCE/DOCKET NUMBER:  P31005C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-270-5024
;      TELEFAX:  610-270-5090
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  382 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-470-299-7

  Query Match             96.9%;  Score 565;  DB 1;  Length 382;
  Best Local Similarity   97.3%;  Pred. No. 5.2e-60;
  Matches  107;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 225

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 275


RESULT 6
US-08-470-299-10
; Sequence 10, Application US/08470299
; Patent No. 5783181
;  GENERAL INFORMATION:
;    APPLICANT:  Browne, Michael J.
;    APPLICANT:  Murphy, Kay E.
;    APPLICANT:  Chapman, Conrad G.
;    APPLICANT:  Clinkenbeard, Helen E.
;    APPLICANT:  Young, Peter R.
;    APPLICANT:  Shatzman, Allan R.
;    TITLE OF INVENTION:  No. 5783181el Compounds
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham Corporation
;      STREET:  709 Swedeland Road, P.O. Box 1539
;      CITY:  King of Prussia
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19406
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,299
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sutton, Jeffrey A.
;      REGISTRATION NUMBER:  34,028
;      REFERENCE/DOCKET NUMBER:  P31005C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-270-5024
;      TELEFAX:  610-270-5090
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  382 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-470-299-10

  Query Match             96.9%;  Score 565;  DB 1;  Length 382;
  Best Local Similarity   97.3%;  Pred. No. 5.2e-60;
  Matches  107;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 APEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 225

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 275


RESULT 7
PCT-US96-13152-4
; Sequence 4, Application PC/TUS9613152
;  GENERAL INFORMATION:
;    APPLICANT:  Martin, Ulrich, et al.
```

; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; ADDRESSEE: Attn: Norman D. Hanson
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13152
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: 27-Dec-95
; APPLICATION NUMBER: EP 95 112 895.8
; FILING DATE: 17-Aug-95
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Norman D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-13152-4

Query Match 96.9%; Score 565; DB 5; Length 443;
Best Local Similarity 97.3%; Pred. No. 6.4e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
|| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 227 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 286

Qy 61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 287 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 336

RESULT 8
US-08-704-744-81
; Sequence 81, Application US/08704744
; Patent No. 5705154
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5.3
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,744
; FILING DATE: 06-SEPT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208886
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: PCT/US/95/02400
; FILING DATE: 08-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: JB0429K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2987
; TELEFAX: (908) 298-5388
; TELEX:
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-704-744-81

Query Match 96.9%; Score 565; DB 1; Length 467;
Best Local Similarity 97.3%; Pred. No. 6.9e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
|| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 251 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 310

Qy 61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 311 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 360

RESULT 9
US-07-916-098A-45
; Sequence 45, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET D.
; APPLICANT: ROSA, JOSEPH J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/916,098A
; FILING DATE: July 24, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:

```
;      APPLICATION NUMBER:  PCT/US91/08843
;      FILING DATE:  No. 5871732ember 27, 1991
;      CLASSIFICATION:  424
;      APPLICATION NUMBER:  07/618,542
;      FILING DATE:  No. 5871732ember 27, 1990
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  JOHN J. MC DONNELL
;      REGISTRATION NUMBER:  26,949
;      REFERENCE/DOCKET NUMBER:  92,310-G
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 715-1000
;      TELEFAX:  (312) 715-1234
;      TELEX:  910/221-5317
;  INFORMATION FOR SEQ ID NO:  45:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-916-098A-45

  Query Match            96.9%;  Score 565;  DB 2;  Length 467;
  Best Local Similarity   97.3%;  Pred. No. 6.9e-60;
  Matches  107;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 311

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 361


RESULT 10
US-08-523-894-8
; Sequence 8, Application US/08523894
; Patent No. 6136310
;  GENERAL INFORMATION:
;    APPLICANT:  Hanna, Nabil
;    APPLICANT:  Newman, Roland A.
;    APPLICANT:  Reff, Mitchell E.
;    TITLE OF INVENTION:  Recombinant Anti-CD4 Antibodies for Human
;    TITLE OF INVENTION:  Therapy
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22314-3187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/523,894
;      FILING DATE:  06-SEP-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Teskin, Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-165
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-836-6620
;      TELEFAX:  703-836-2021
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-523-894-8

  Query Match            96.9%;  Score 565;  DB 3;  Length 467;
  Best Local Similarity   97.3%;  Pred. No. 6.9e-60;
  Matches  107;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 310

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 360


RESULT 11
US-08-523-894-10
; Sequence 10, Application US/08523894
; Patent No. 6136310
;  GENERAL INFORMATION:
;    APPLICANT:  Hanna, Nabil
;    APPLICANT:  Newman, Roland A.
;    APPLICANT:  Reff, Mitchell E.
;    TITLE OF INVENTION:  Recombinant Anti-CD4 Antibodies for Human
;    TITLE OF INVENTION:  Therapy
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22314-3187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/523,894
;      FILING DATE:  06-SEP-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Teskin, Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-165
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-836-6620
;      TELEFAX:  703-836-2021
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-523-894-10

  Query Match            96.9%;  Score 565;  DB 3;  Length 467;
  Best Local Similarity   97.3%;  Pred. No. 6.9e-60;
  Matches  107;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 APEFGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 310

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 360


RESULT 12
```

```
US-08-523-894-12
; Sequence 12, Application US/08523894
; Patent No. 6136310
;  GENERAL INFORMATION:
;    APPLICANT:  Hanna, Nabil
;    APPLICANT:  Newman, Roland A.
;    APPLICANT:  Reff, Mitchell E.
;    TITLE OF INVENTION:  Recombinant Anti-CD4 Antibodies for Human
;    TITLE OF INVENTION:  Therapy
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22314-3187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/523,894
;      FILING DATE:  06-SEP-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Teskin, Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-165
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-836-6620
;      TELEFAX:  703-836-2021
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-523-894-12

  Query Match             96.9%;  Score 565;  DB 3;  Length 467;
  Best Local Similarity   97.3%;  Pred. No. 6.9e-60;
  Matches  107;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 APEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 310

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 360


RESULT 13
US-08-070-116A-4
; Sequence 4, Application US/08070116A
; Patent No. 5885573
;  GENERAL INFORMATION:
;    APPLICANT:  Zivin, Robert A.
;    APPLICANT:  Jolliffe, Linda K.
;    APPLICANT:  Bluestone, Jeffrey A.
;    TITLE OF INVENTION:  Methods and Materials For Modulation
;    TITLE OF INVENTION:  of the Immunc-suppressive Activity and
;    TITLE OF INVENTION:  Toxicity of Monoclonal Antibodies
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/070,116A
;      FILING DATE:  01-JUN-1993
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wilson, Mark B.
;      REGISTRATION NUMBER:  37,259
;      REFERENCE/DOCKET NUMBER:  ARCD:082
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  109 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-070-116A-4

  Query Match             96.2%;  Score 561;  DB 2;  Length 109;
  Best Local Similarity   97.2%;  Pred. No. 2.9e-60;
  Matches  106;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 PPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 61
              |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 60

Qy         62 REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109


RESULT 14
US-08-557-050-4
; Sequence 4, Application US/08557050
; Patent No. 6491916
;  GENERAL INFORMATION:
;    APPLICANT:  Bluestone, Jeffrey A.
;    APPLICANT:  Zivin, Robert A.
;    APPLICANT:  Jolliffe, Linda K.
;    TITLE OF INVENTION:  METHODS AND MATERIALS FOR MODULATION OF
;    TITLE OF INVENTION:  THE IMMUNO-SUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
;    TITLE OF INVENTION:  ANTIBODIES
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/557,050
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/06198
;      FILING DATE:  01-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/070,116
;      FILING DATE:  01-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wilson, Mark B.
```

```
;      REGISTRATION NUMBER:  37,259
;      REFERENCE/DOCKET NUMBER:  ARCD:208
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  109 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-557-050-4

  Query Match             96.2%;  Score 561;  DB 4;  Length 109;
  Best Local Similarity   97.2%;  Pred. No. 2.9e-60;
  Matches  106;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 PPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 61
              |   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 60

Qy         62 REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109


RESULT 15
US-08-808-720-3
; Sequence 3, Application US/08808720
; Patent No. 6100387
;  GENERAL INFORMATION:
;    APPLICANT:  Herrmann, Steve
;    APPLICANT:  Swanberg, Stephen
;    TITLE OF INVENTION:  CHIMERIC POLYPEPTIDES CONTAINING
;    TITLE OF INVENTION:  CHEMOKINE DOMAINS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Insititute, Inc.
;      STREET:  87 CambridgePark
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/808,720
;      FILING DATE:
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sprunger, Suzanne
;      REGISTRATION NUMBER:  P-41,323
;      REFERENCE/DOCKET NUMBER:  GI5291
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8284
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  326 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-808-720-3

  Query Match             95.9%;  Score 559;  DB 3;  Length 326;
  Best Local Similarity   96.4%;  Pred. No. 2.3e-59;
  Matches  106;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
              ||  |  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 APEFEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 169

Qy         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 219

Search completed: April 29, 2004, 08:47:44
Job time : 17.5 secs
```